Perfect score: Sequence: Scoring table:

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Sequence 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 2, Appliance 3, Applia
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Sequence 2, Appli
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2000-01-26
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TYPE: PRT
ORGANISM: Erwinia amylovora
        PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-0
NUMBER OF SEQ 1D NOS: 26
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PCT-US01-02579-3
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2, 2002, 03:27:49 ; Search time 139.22 Seconds (Without alignments) 1095.460 Million cell updates/sec
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core greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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2079
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Score Match Length DB
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Length 403;

Score 2079; DB 1; Pred. No. 1.6e-169;

100.0%;

Query Match Best Local Similarity

Sequence 3, Appl1

PCT-US01-02579-3

403 100.0 2079

ID

Result

Description

us-09-770-693-3.rapm

0; Query Match Rest Local Similarity Matches 403; Conset	Qy 1 MSLATSGLGASTW 	Qy 6.1 TGMMNOMSMMGG 	Qy 121 TESTINSPLDGAL 	Qy 181 QGSSSGGKQPTEG 	Qy 241 GGKGLQNLSGPVI 	Qy 301 GQFMDQYPEVFGR	Qy 361 PMAGDYGNGNLQP 	PRESENT 3 107-12 PRESENT INFORMATION TO SERVICE STATE	; STRANDEDNESS:
Matches 403; Conservative 0; Mismatches 0; Index 0; Gaps QY 1 NSIAMYSGLANFWISTGGARGHARTLGTSRQNAGLGGSRSALGLGGGARGHARTLGTSRQNGTAGLGGSRSALLGTSRQNAGLGGSRSALGLGGSRSQCTATSRQNAGLGGSRSALGGGGSRSQCTATSRQNAGLGGSRSALGGGGGSRCALGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Oy 61 TOMMOMMENMOSOGILMOGILMOGILGOGILGOGILGOGILGOGILGOGILG	OY 121 TTSTTNSPLDQALGINSTSONDGTSGTDSTSDSGDWQQLLKNFSEIMQSLRGDQDGGT 180	Oy 181 OGSSSGGROPTBGBONAVKROPTDALSGLMCNGL&OLLGNGGLGGGGGGGNAGTGLGGSSL 240 111 [111111111111111111111111111111111	OY 241 GCRGLONLSGPVDYOQLGNAVGTGLGWAGIQALMDIGTHRIBSTRSFYNKGDRAMAKEI 300 THITIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 301 GOPMOOYPEVPGREOTOKGFGOEWTDOKSHARALSKRODOGMTPASHEDPNKAKCHIKR 360 101 GOPMOOYPEVPGKOOYGKGFGOEWTDOKSHAKALSKRODOGMTPASHEDNKAKCHIKR 360 301 GOPMOOYPEVPGKOOYGKGFGOEWTDOKSHAKALSKRODOGMTPASHEDNKAKCHIKR 360	Oy 361 PHACDTONONICARGAGGSSLCIDAMAGDAINNALCKIGAA 403 	RESULF 2 2 FOTT-UGSY-2459-3 Qualence 3, Application Pc/TUGS722629	APPLICATE OF THE INTERCENT OF THE INTERC	PCT-US97-22629-3

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GGLMGGGLGGGLGMGLGGSGGLGEGLSNALNDMLGGSLNTLGSKGGNN 120
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100.0%; Score 2079; DB 1; Length 403; 100.0%; Pred. No. 1.6e-169; Live 0; Mismatches 0; Indels 0;
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N: ENHANCEMENT OF GROWTH IN PLANTS
ES: 10
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on Square, P.O. Box 1051
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Compatible
SM: PC-1005/MS-100
SM: PC-1005/MS-100
SM: Release #1.0, Version #1.30
MB DAT.
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MICHAEL 30,727

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DMBER: US 60/036,048
27-JAN-1997
INFORMATION:
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121 TISTINSPLDQALGINSTSQNDDSTSGTDSTSDSSDPMQQLLKMFSEIMQSLFGDGQDGT 180
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                                                                                                                                                                                         100.0%; Score 2079; DB 1; Length 403;
100.0%; Pred. No. 1.6e-169;
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APPLICANT: Laby, Non J.
TITLE OF INVENTION: ELLCITOR OF THE HYPERSENSITIVE RESPONSE
TITLE OF INVENTION: IN PLANTS
                                                                                                                                                                                                                                0: Indels
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SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
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STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                    0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION WUMBER: •US 08/200,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08851376
GENERAL INFORMATION:
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APPLICANT: Bauer, David W.
APPLICANT: Beer, Steven V.
APPLICANT: Collmer, Alan
SERGUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
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Best Local Similarity 100.0
Matches 403; Conservative
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CORRESPONDENCE ADDRESS:
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PCT-US98-03604-3
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New York
NY: U.S.A.
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                                                                                          TOPOLOGY:
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                                                                                                                                                                                             1 MSLNTSGLGASTWQISIGGAGGNNGLLGTSRQNAGLGGGNSALGLGGGGNQNDTVNQLAGLL 60
                                                                                                                                                                                                                            1 MSLATSGLGASTMQ1S1GGAGGNNGLLGTSRQNAGLGGNSALGLGGGNQNDTVNQLAGLL 60
                                                                                                                                                           O: Gaps
                                                                                                           Query Match 100.09; Score 2079; DB 1; Length 403; Best Local Similarity 100.09; Pred. No. 1.6-169; Matches 403; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.58equence 1. Application Pc/TUS9803604
Sequence 1. Application Pc/TUS9803604
APPLICANT: Cornell Research Foundation, Inc.
APPLICANT: Cornell Research Foundation, Inc.
APPLICANT: GOTHER RESEARCH RESPONSE ELICTION FILES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 PMAGDIGNGNEQARGAGGSSLGIDAMMAGDAINNMALGKEGAA 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: P.O. Box 1051, Clinton Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1522
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/039,226
FILING DATE: 28-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Goldman, Michael L. REGISTRATION NUMBER: 30,7
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                         MOLECULE TYPE: protein
PCT-US98-01507-3
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CORRESPONDENCE ADDRESS:
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U.S.A.
            TOPOLOGY: linear
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WARRICHAM-MAN, Remail J. T. SPERICHAM-MAN, REMAINS BELICITOR BERT, ZEROR V. APPRILOZH: BERT, ZEROR V. APPRILOZH: TITLE OF INVESTION: PRESENSITIVE RESPONSE ELICITING A HYPERSENSITIVE RESPONSE AND USESTITLE OF INVESTION: THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ucery match 100.0%; Score 2079; DB 14; Length 403; Best Local Similarity 100.0%; Pred. No. 1.66-169; Matches 403; Conservative 0; Mismarraka.
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: Clinton Square, P.O. Box 1051
Rochester
                                                                                                                                    TORREY AMEN AMENONEL L.
NAME: Goldman, Michael L.
REGISTRATION UNBERR: 30,727
            APPLICATION NUMBER: US/09/030,270
                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,226
FILING DATE: 28-FEB-1997
ATTORNEY/AGENT INFORMATION:
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GENERAL INFORMATION:
                                                                                                                                                                                     REFERENCE/DOCKET HUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPRA: (716) 263-1304
INFORMATION FOR ESD 1D NO: 3:
                                                                                                                                                                                                                                                                                                                 : 403 amino acids
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MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                     LENGTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zitter, Thomas A.
APPLICANT: Zitter, Thomas A.
TITLE OF INVENTION: INSECT CONTROL WITH A
TITLE OF INVENTION: HYPRSENSITIVE RESPONSE ELICITOR
WHORER OF SUGNETION: HYPRESENSITIVE RESPONSE ELICITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36I PMAGDTGNGNLOARGAGGSSLGIDAMMAGDAINNMALGKIGAA 403
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: P.O. Box 1051, Clinton Square
Rochester
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide
US-08-851-376-2
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MEDIUM TYPE: Floppy
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14603
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121 TISTINSPLDQALGINSTSQNDDSTSGTDSTSDSSDPMQQLLKMFSEIMQSLFGDGQDGT 180
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PAULOANT: SCHALING, MICHAEL HIVE RESPONSE ELICITOR-INDOCED STRISSS TITLE OF INDOCED STRISSS TITLE OF INDOCED STRISSS TITLE STRISBERGE: 133.4741 (RE-CO)3

CORREST PAULOANTS OF STRISBERGE: 105.09.4741.614

CORREST PAULOANTS OF STRISBERGE: 105.09.4741.614

DARREST PAULOANTS STRISBERGE: 105.09.4741.614

DARREST PAULOANTS STRISBERGE: 1995-110.0
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CURRENT APPLICATION NUMBER: US/09/412,100
CURRENT FILING PARE: 1959-10-04
DARLIER FILING NUMBER: 60/10,050
RARLIER FILING NUMBER: 60/10,050
RARLIER FILING NUME: 1998-10-05
SOFFWHARE: PARENTING NUMBER: 2.0
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US-09-431-614-3
; Sequence 3, Application US/09431614
; GENERAL INFORMATION:
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                                                                                                                                                                                                                             ) ORGANISM: Erwinia amylovora
US-09-412-100-23
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121 TTSTTNSPLIDQALGINSTSQNDSTSGTDSTSSSDBPAQQLKHFSEINGSLFGDGDGT 180
122 TTSTTSTLDQALGINSTSQNDGTSGTDSTSSSDBAQQLKHFSEINGSLFGDGDGT 180
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                                                                                                                                                                                                                                                                                                                                                           NAME: Coldman, witched; L., REGISFRATION WITCHED; 30,727 REFERENCE/DOCKET NUMBER: 19603/1301 FTELEDOMONICATION INFORMATION: TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/048,109
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                  APPLICATION NUMBER: US/09/086,118
                                                              NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
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; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                  SOFTWARE: Patentin Rel
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US-09-086-118-23
                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                           COMPUTER READABLE FORM:
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                                                                   1131 TISTINSPLOQALGINSTSQNDSSTSGTSSSSDPMQQLLKMFSELMQSLFGDGQDGT 180
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                                                    TOWNSHINGGGGLAGGGLANGLAGGGLANGLAGGGLANALNDMLAGGLATTLASKAGNN 120
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1 MSLNTSGLGASTWOISIGGAGGNNCLLGTSRONAGLGGNSALGLGGGNDNDTVNQLAGLL 60
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CHRESEPORDERICE ADDRESS

CHRESTESSER INVENT INSTITUTE DEVINE & DOYLE LIP

STREET: CLINICAL SIGNARE, P.O. BOX 1051
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         361 PMAGDIGNGNLQARGAGGSSLGIDAMMAGDAINNWALGKLGAA 403
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REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/597,840
FILING DATE: 20-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 09/013,587
FILING DATE: <Unknown>
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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GENERAL INFORMATION:
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STRANDEDNESS: <Unknown>
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SEQUENCE CHARACTERISTICS:
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COUNTRY: U.S.A.
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                                                       Gaps
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Query Match 100.0%; Score 2079; DB 19; Length Best Local Similarity 100.0%; Pred No. 1.6e-169; Matches 403; Conservative 0; Mismatches 0; Indels Matches 403; Conservative 0; Mismatches 0; Indels
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1996-12-05
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SOFTWARE: PatentIn Ver. 2.1
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US-09-766-348-3
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PRIOR FILING DATE: 1996-1
Query Match
Best Local Similarity
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APPLICANT TEAL BOTH TEAL B
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                                                                                                                                                                                                                                                                                                    121 TISTINSPLDGALGINSTSQNDSTSGTDSTSDSNOOLLKWFSELWGSLEGDGORGT 180
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                                                                                                                                                                                                                                                  1 MSLATSGLGASTWQISIGGAGGNNGLLGTSRQNAGLGGNSALGLGGGGNQNDTVNQLAGEL 60
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                                                                                                                                                  ; Score 2079; DB 22; Length 403;
; Pred. No. 1.6e-169;
0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLUBERT PRESENCE: 7.129/3/10
CLUBERT FILMS OATS: 7.01-06-13
CLUBERT FILMS OATS: 7.001-06-13
PRIOR FILMS OATS: 2.001-06-13
NUMBER OF SEQ ID NOS: 16
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09880371
                                                                                                                                                      100.0%;
                                                                         ; ORGANISM: Erwinia amylovora
US-09-879-248-3
                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 403; Conservative
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US-09-880-371-3
SOFTWARE: Patentin Ver.
SEQ ID NO 3
                                      LENGTH: 403
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US-09-880-371-3
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                                                         TYPE - PRT
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APPLICANT CONCENSOR, FERDERS
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TITLE OF INVENTION. FROM THE GROWNE OF A NECERCIBELHY USING A RAC-BASED
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TITLE OF INVENTION DAY, ADI-COLE CONCENSOR APPLICANT CONTENSOR 
sequence 1, App11
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sequence 217, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 SGLGASTMQISIGGAGGNNGLLGTSRQNAGLGGNSALGLGGGGNQNDTVNQL----AGLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 GHGGTGGLSTNGDG----GVGGAGGNAGMLAGPGGAGGAG-----G
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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
209-673-476-727
Sequence 727, Application US/09673476
GENERAL INFORMATION:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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(without alignments)
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| Adding 
                                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                6 SGLGASTMQISIGGA-GGNNGLLGTSRQNAGLGGNSALGLGGGNQNDTVNQLAGLLTGNM 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Score 174.5; DB 6; Length 440;
, Pred. No. 3.4e-06;
37; Mismatches 141; Indels 111;
                                                                                                                                                                                                                                                                                       . 29
                                                                                                                                                                                                                        Ouery Match
9.2%; Score 191.5; DB 5; Length 255;
BB 5 seek Local Similarity 28.8%; Pred No. 11e-07;
Matches 78; Conservative 13; Mismatches 113; Indels 67;
Matches 78; Conservative 13; Mismatches 113; Indels 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 LGGKGLQNLSGPVDYQQLGNAVGTGIGMKAG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 GGGGGYAAASG-----YGHGGGAGGEGSG 251
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                                                                                               , ORGANISM: Arabidopsis thaliana
US-09-573-6558-1638
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Best Local Similarity 23.9%;
Matches 91; Conservative 37
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ORGANISM: Homo sapiens
US-10-006-063A-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-006-063A-52
SEQ ID NO 1638
LENGTH: 255
                                                                     TYPE: PRT
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TITLE OF INVENTION: Thereby FILE REPRESENCE: 2750-080769
                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
      228 DGGAGGNAGLLLSSGGAGGGGGFGTAGGV----GGAGGNAGWLGFGGAGGVGGSAGL-- 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ----TGMMMAMASMAGGGGLMGGGLGGGLG----NGLGGSGGLGEGLSNALNDMLGGSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 NTLGSKGGNNTTSTINSPLDQALGINSTSQNDDSTSGTDSTSDSSDPMQQLLKMFSEIMQ 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 -LGGDGGAGGNAGLILSSGGAGGFGGFGAGGVGGAGGNAGWLGFGAGGIGGIGGGNANGG 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 AGGNGGTGGOLMGS --GGAGVEGGAA----LSVGDTGGAGGVGGSAGL-----IGT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 9.6%; Score 199.5; DB 5; Length 334; Bert Local Smilarity 30.4%; Pred. No. 18e-08. Matches 90; Conservative 16; Mismatches 101; Indels 89;
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CURRENT FILMO DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 3281
SOFTWARE: Patentin version 3.0
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) Sequence 1638, Application US/09573655B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                           , ORGANISM: Mycobacterium sp.
US-09-673-476-728
                                                                                                     274 LNDIGT 279
                                                                                                                                                        281 --- IGT 283
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LRNGTH; 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 GNSAGSFGMNPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNONEGCTNPPPSGS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 DSTSDSSDPMQQLLKMFSEIMQSLFGDGQDGTQGSSSGGKQPTEGEQNAYKKGVTDALSG 208
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                                    238 GGGSSNS-----NGSSSG 270
                                                                                                                                         209 LHGNGLSQLLGNGGLGGGGGGGNAGTGLDGSSLGGKGLQNLSGPVDYQQLGNAVGTGIGM- 267
                                                                                                                                                                                            271 GSSSGSSSGGSSGGSSGGS-SGNSGGSRQDSGSESWGSSTGSSSGNHGGSGGGNG 329
                                                                                                                                                                                                                                                                                          268 ------KAGIQALNDIGTHRHSSTRSFVNKGDRAMAKEIGQFWDQYPEVF 311
                                                                                                                                                                                                                                                                                                                                                           330 HXPGCEMPGNEARGSGESGIQGFRGGGV--SSNMREISKEGNRLLG------ 373
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149 DSTSDSSDPMQQLLKMPSRIMQSLFGDGQDGTQGSSSGGKQPTEGDQNAYKKGVTDALSG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                           312 GKPOYOKGPGOEVKTDDKSW 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 -----GSGDNYRGQGSSW 386
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Eaton, Dan 1.
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US-10-006-130A-52
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US-10-006-130A-52
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              121 IRRGADAVRGSWGSVPGHSGAWETSGGHGIFGSQGGLG---GGGGGNPGGLGTPWVHGYP 177
                                                                                                                                                                                     178 GNSAGSFGMNPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGS 237
                                                                                                                                                                                                                                                                    149 DSTSDSSDPWQQLLKMFSEIMQSLFGDGQDGTQGSSSGGKQPTEGEQNAYKKGVTDALSG 208
                                                                                                                                                                                                                                                                                                                                                                                                              209 IMCNGLSQLLGNGGLGGGGGGNAGTGLDGSSLGGKGLQNLSGPVDYQQLGNAVGTGIGM- 267
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                                                                                                                           104 DMLGGS---LWTLGS---KGGNN-----TTSTTNSPLDQALG-INSTSQNDDST----SGT 148
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Best Local Similarity 23.9%; Pred. No. 3.4e-06;
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PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 477
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CURRENT APPLICATION NUMBER: US/10/006,117A
CURRENT FILING DATE: 2002-03-19
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Fong, Sherman
Gao, Wei-Giang
Goddard, Audrey
Goddwski, Paul J.
Grimaldi, Christopher J.
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GENERAL INFORMATION:
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Hillan, Kenneth J.
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan 1.
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US-10-006-117A-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 -----KACIQALNDIGTHRHSSTRSFVNKGDRAMAKEIGQFMDQYPEVF 311
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                      53 VNQLAGLLTGNMM--------MMSNMGGGGLMG--GGLGGGLGNGLGGSGGLGEGLSNALN 103
                                                                          178 GNSAGSFGMNPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGS 237
                                                                                                                                                                          104 DMLGGS--LNTLGS---KGGNN----TISTINSPLDQALG-INSTSQNDDST----SGT
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Eaton, Dan 1.
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PRIOR PRICERION PRINCIPLE 1899-10-10

PRIOR PRILICANDE NAMER: 650-0220

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PRIOR PRILICANDER: 1898-00-10

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FILING DATE: 1998-10-28
APPLICATION NUMBER: 60/106029
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Matches
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178 GNSAGSFGMNPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNBGCTNPPPSGS 237

.04 DMLGGS--LNTLGS---KGGNN-----TTSTTNSPLDQALG-INSTSONDDST----SGT 148

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61 GAAGSKVSBALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDV 120

9 GASTMQISIGGAGGNNGLLGTS-RQNAGLGGNSALG------LG-----GGNQNDT 52

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FILING DATE: 1998-09-10

18-09-770-693-3.raph

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APPLICANT: Pan. James APPLICANT: TITLE OF INVENTION: Secreted and Transmembrane Polypoptidus and Nucleic TITLE OF INVENTION: APPLICANT: PASSIONET ON A FACIGE Exponding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 GNSAGSFGMNPQGAPWGGGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNBGCTNPPPSGS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 DSTSDSSDPWQQLLKHFSEIWQSLFGDGQDGTQGSSSGGKQPTEGEQNAYKKGVTDALSG 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 IRHGADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLG---GGGGGNFGGLGTPWVHGYP 177
                                                                                                                                                           Indels 111; Gaps
                                                                                                                                                                                                                                         9 GASTWQISIGGAGGNNGLLGTS-RQNAGLGGNSALG-----LG-----GGNQNDT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 GGGSSNS -----SGGSGSGSGSGSGSGSGSNN -----NGBSSG
                                                                             Length 440;
                                                                             Query Match 8.4%; Score 174.5; DB 6; Best Local Smilarity 23.9%; Pred. no. 3.4e-06; Matches 91; Conservative 37; Mismatches 141;
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CURRENT FILING DATE: 2001-12-13
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
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PRIOR APPLICATION NUMBER: 60/106029
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Fong, Sherman
Gao, Wel-Qiang
Goddard, Audrey
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APPLICANT: Botstein, David
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                                                   RELOR MELLOR TOTAL MARSHES 667, 2024 OF RELOR MELLOR MARSHES 667, 2024 OF RELOR MARSHES 667, 2024 OF RELOR MARSHES 67, 2023 OF RELOR MARSHES 67, 2024 OF RELOR MARSHES 67, 202
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APPLICATION NUMBER: 60/106023
FILING DATE: 1998-10-28
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APPLICATION NUMBER: 60/105169
FILING DATE: 1998-10-22
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PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
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PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/105881
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PRIOR APPLICATION NUMBER: 60/104987
PRIOR FLIKED DATE: 1998-10-20
PRIOR FLIKED DATE: 1998-10-20
PRIOR PLICATION NUMBER: 60/105000
PRIOR FLIKED DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR PLICATION NUMBER: 60/105002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 DSTSDSSDPWQQLLKNFSEIMQSLFGDGQDGTQGSSSGGKQPTEGEQQNAFKKGVTDALSG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 GGGSSNS-----NGSSSSSGSQSGSGSGSGSGSGS--SNGDNN-----NGSSSG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 LMGNGLSQLLGNGGLGGGGGGRAGTGLDGSSLGGKGLQNLSGPVDYQQLGNAVGTGIGM- 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 ------KAGIQALNDIGTHRHSSTRSFVNKGDRAMAKEIGQFMDQYPEVF 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 HKPGCEKPGNEARGSGESGIQGFRGQGV--SSNAREISKEGNRLLG------ 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 IRHGADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLG----GQGQGNPGGLGTPWVHGYP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 DMLGGS--LNTLGS---KGGNN-----TTSTTNSPLDQALG-INSTSQNDDST----SGT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 GNSAGSFGMNPQGAWGQGGNGGPPNFCTNTQGAVAQPGYGSVRASNQNBGCTNPPFSGS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GAAGSKVSEALGOGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 VNQLAGLLTGNAM------PAKSMAGGGGLMG--GGLGGGGLGNGLGGSGGLGEGLSNALN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 111; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 GASTMQISIGGAGGNNGLLGTS-RQNAGLGGNSALG-----LG-----GGNQNDT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 440;
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NUMBER OF SEQ ID NOS: 477
SEQ ID NO 52
                                               CURRENT FILMN DATE: 2001-12-06
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ 1D NOS: 477
SEQ ID NO 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.4%; Score 174.5; DB 6;
23.9%; Pred. No. 3.4e-06;
ative 37; Mismatches 141;
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CURRENT APPLICATION NUMBER: US/10/006,041A
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PRICANT POR, Sherman
PRICANT COOK, Sherman
PRICANT Godderd, Audrey
APPLICANT Godderd, Audrey
APPLICANT Godderd, Audrey
APPLICANT Grimaldi, Christopher J.
APPLICANT Grimaldi, Christopher J.
APPLICANT BLIMAN, Kenneth J.
APPLICANT: Hillan, Kenneth J.
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Eaton, Dan 1.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 3.4e-06;
37; Mismatches 141; Indels 111; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 GASTMQISIGGAGGNNGLLGTS-RQNAGLGGNSALG-----LG-----GGNONDT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6; Length 440;
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                  RECOR PRIZING DATE: 1811-7. IN SECONDARY OF 
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; Sequence 52, Application US/10006041A
; GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
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APPLICANT: BOCKELIN, DEVID
APPLICANT: Desnoyers, Louc
APPLICANT: Ration, Dan 1.
APPLICANT: Retrara, Napoleone
APPLICANT: FORGY, Sherman
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Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91; Conservative
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US-10-006-818A-52
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18:
Ouery Match 8.48; Score 174.5; DB 6; Jength 440; Best Local Similarity 22.94; Pred. No. 3.4e-06; G. Mester Matches 141; Conservative 37; Kismatches 141; Indels 111; Gaps
                                                                                                                                         61 GAAGSKVSEALGGGTREAVGTGVRQVPGPGAADALGNRVGBAAHALGNTGHEIGROAEDV 120
                                                                                                                                                                                                                                    121 IRHGADAVRGSWGGVPGHSGANETSGGHGIFGSQGGLG---GQGQRNPGGLGTPWHGFP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 GGGSSNS-----NGSSSGSGSGSGSGSGSGSGS--SNGDNN-----NGSSSG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pan, James
APPLICANT: Pan, Micholas F.
APPLICANT: Pan, Micholas F.
TITLE OF INVENTION: Socreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                         53 VNQLAGLLTGMAM-------MASNANGGGGLKG--GGLGGGLGNGLGGSGGLGEGLSNALN 103
                                                                                                                                                                                                                                                                                                                   104 DMLGGS--LNTLGS---KGGNN----TTSTTNSPLDQALG-INSTSQNDDST----SGT 148
                                                                                                                                                                                                                                                                                                                                                                   178 GNSAGSFGMNPQGAPWGQGGNGCPPNFGTWTQGAVAQPGYGSVRASNQNEGCTNPPPSGS 237
                                                                                                                                                                                                                                                                                                                                                                                                                        149 DSTSDSSDPMQQLLKMFSEINQSLFCDGQDGTQGSSSGGKQPTEGEGQNAYKKGVTDALSG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 IMCHGLSQLLGNGGLGGGGGNAGTGLDGSSLGGKGLQNLSGPVDYQQLGNAVGTGIGM- 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 HKPGCEKPGNEARGSGESGLOGFRGOGV--SSNWRELSKBGNRLLG----------373
                                                                                                          9 GASTMQISIGGAGGNNGLLGTS-RQNAGLGGNSALG------LG------GGNQNDT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.48; Score 174.5; DB 6; Length 440; Best Local Similarity 23.94; Pred, No. 3.4e-06; Matches 91; Conservative 37; Mismatches 141; Indels 111; Gaps
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NUMBER OF SEQ ID NOS: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: P2830PIC20
CURRENT APPLICATION NUMBER: US/10/012,121A
CURRENT FILING DATE: 2001-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfara, Napoleone
Fong, Sherman
Goo, Wel-Olang
Goddard, Audrey
Goddard, Audrey
Grimaldi, Christopher J.
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GRUBALL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Bestetin, David
APPLICANT: Desnoyers, Luc
APPLICANT: Bacon, Dan 1.
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Hillan, Kenneth J.
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US-10-012-121A-52
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104 DMLGGS--LNTLGS---KGGNN-----TTSTINSPLDQALG-INSTSQNDDST----SGT 148
                                                                                             178 GNSAGSPGNNPQGAPWGGRPNPGTNTQGAVAQPGYGSVRASNQNBGCTNPPPSGS 237
                                                                                                                                                                                                                                                                           149 DSTSDSSDPMQQLLKMPSEIMQSLFGDGQDGTQGSSSGGKQPTEGEQNAYKKGVTDALSG 208
                                                                                                                                                                                                                                                                                                                                              209 IMGNGLSOLLGNGGLGGGGGGNAGTGLDGSSLGGKGLONLSGPVDYQQLGNAVGTGIGN- 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 GSSSGSSSGSSSGGSSGGSSGGS-SGNSGGSRGDSGSBSSWGSSTGSSSGNHGGSGGGNG 329
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POPLICART: Pan, James
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE REFERENCE: P330PLICS:
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8.4%; Score 174.5; DB 6; Length 440;
Bost Local Similarity 23.9%; Pred. No. 3.4e-04; Indels 111; Gaps
Matches 91; Conservative 37; Mismatches 14; Indels 111; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 HKPGCEKPGNEARGSGESGIQGFRQQGV--SSNMREISKEGNRLLG------ 373
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CHERREY TILMNO DATE: 2001-12-12
CHOIS APPLIAND DATE: 2001-12-12
CHOIS APPLIAND LATE AND THE APPLIAND THE WARREN OF SEQ ID NOS: 477
LEAVETH: 4400
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PRILOAM BASE, DESIL P.
PRILOAM BENEATH, DAVID
PRILOAM BENON, DE IL
PRILOAM BENON, DE IL
PRILOAM BONN, WELL DIAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 GRPOYOKGPGOEVKTDDKSW 331
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121 IRBGADAVRGSWQCVPGHSGAWETSGGHGIPGSQGGLG---GQGQGNPGGLGTPWWGYP 177

9 GASTMQISIGGAGGNNGLLGTS-RQNAGLGGNSALG-----LG-----GGNQNDT 52

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18;

9 GASTWOISIGGAGGNNGLLGTS-RQNAGLGGNSALG-----LG-----GGNQNDT 52

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us-09-770-693-3.rapn

Db 178 GNSAGSFGMRPGAPAGGGPRPGGPPTPTGAAVAQFGSGSVARGNBGCFNPPFGG 237	
149 DSTSDSDPWQQLLKMFSELWGSLFQDQDQPQSSSGGKPFBGGWAYKKGVTDALSG 208 138 GQGSSNS -	Oy 268H. AGGOLANDIGHHRISTERSPWAKDRAMAKELOOPMOVPEWF 3111 11 11 11 11 11 11 1
209 LMGNGLSQULGNGGLGGGQQGDNGTGLDGSSLGGRQLQNLSGPVDXQQLGNRVGTG1GM- 267 271 GSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGSSGSSGS	Qy 312 GKPQYQKQRQQQVKTDDKSM 331 Db 374
268	Search completed: May 2, 2002, 03:36:03 Job Lime: 268 sec
312 GROYORGRODEWITDRSH 331 374GSGDNYROQSSH 386	
RESULT 15 10-01-187-52 10-01-187-52 10-01-187-52 10-01-188-188-18-18-18 10-01-188-188-18-18-18-18-18-18-18-18-18-18-	
APPLICANT: Foods, Stemmen MATCHART: Foods, Stemmen MATCHART: Foods, Stemmen APPLICANT: Codesel, Fabl J. APPLICANT: Coffeed, Fabl J. APPLICANT: Corners, Control Control Control APPLICANT: Corners, Control APPLICANT: Corners, Areast L. APPLICANT: Granter, Corners, Areast L. APPLICANT: HILLON Formeth J.	
APPLICANT: Foun James F. APPLICANT: Foun, Micholas F. TITES OF WINNERTON: Secreted and Transmembrane Polypeptides and Nucleic FILE OF WINNERTON: Acids Recording the Same CHERGENSPERTON: ACIds Recording the Same CHERGENSPERTON: ACIDS MICHOLAGES IN SCHOOL CHERGENSPERTON ACIDS AND TANKER. 1951/1913.387A	
And the Republic Control of the Cont	
7 YYPS: RPT (Memo sapitens (US-10-015-387A-52	
Query Match 8.41, Score 174.5; DB 6; Length 440; Best Local Similarity 23.49; Pered No. 34-6-06; Bast Local Similarity 23.49; Pered No. 34-6-06; Bast Conservative 37; Mismarches 141; Indels 111; Gaps 18;	
9 GASTWOISIGGAGGNRGLLOTS-ROHACLGONSALG	
53 VNOLAGLITGARM	
104 DRILGGS-LAPIGSKGGNATSSTNSFLDGALG-INSTSGADSTSCT 1148 178 GNSAGSFDARPQASFPOARGEPRATOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTO	
149 DSTSDSSDPMQQLAKMF8ENDGLFGDQDDGTQGSSGGKQFTBGBQNAYKKGVTDALSG 208 1 	
209 IMGNSISQLIGNGGIGGGGGGAAGTGIDGSSLGGKGIQNLSGPVDYDQIGAAVGTGIGM- 267	

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(2012, 4) Proteins A. Dipatol Senial Combines and Compiler A. Commission and Compiler A. C
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/cgn2_6/ptodata/1/pna/US09_MERGED_COMB.seq4:*
/cgn2_6/ptodata/1/pna/US09_MERGED_COMB.seq4:*
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/cgn2_6/ptodata/1/pna/USO6_NERGED_COMB.seq1:*
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/cgn2_6/ptodata/1/pna/USO9_NERGED_COMB.seq1:*
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/cgn2_6/ptcdata/2/pna/US6012_COMB.seg
/cgn2_6/ptcdata/2/pna/US6013_COMB.seg:
                  May 2, 2002, 03:37:15 ; Search time 3673.21 Seconds (Without alignments) 7556.017 Willion cell updates/sec
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                                                                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                       OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

Result

/cqn2_6/ptodata/1/pna/PCT_MERGED_COMB.seq1:*

NO.	Score	Match	Match Length DB	98	10	Description
-	1288	100.0	1288	H	PCT-US01-02579-4	÷
100	1288	100.0	1288	7	PCT-US97-22629-4	Sequence 4, Appli
. ~	1288	100.0	1288	-	PCT-US98-01507-4	÷
4	1288	100.0	1288	-1	PCT-US98-03604-4	Sequence 4, Appl1
'n	1288	100.0	1288	12	US-08-851-376-3	σ.
9	1288	100.0	1288	14	US-09-030-270-4	4
7	1288	100.0	1288	14	US-09-086-118-24	~
- 00	1288	100.0	1288	18	US-09-412-100-24	Sequence 24, Appl
o	1288	100.0		18	US-09-431-614-4	Ą,
2	1288	100.0		22	US-09-597-840-4	Ą,
Ξ	1288	100.0	1288	30	US-09-766-348-4	÷
12	1288	100.0		30	US-09-770-693-4	÷
13	1288	100.0		31	US-09-835-684-4	÷
Z	1288	100.0		31	US-09-879-248-4	÷
15	1288	100.0		31	US-09-880-371-4	÷
19	1288	100.0		67	US-10-010-390-4	÷
13	1288	100.0		67	US-10-034-158-4	Sequence 4, Appli
18	1288	100.0		68	US-09-691-682-3	'n
61	1269.6	98.6		٣	US-07-907-935A-3	m,
50	1269.6	98.6		9	US-08-200-724-3	'n
21	1209	93.9		12	US-08-851-376-4	Sequence 4, Appli
22	1209	93.9		9	US-09-691-682-4	÷
23	1147	89.1		00	US-08-475-775A-4	÷
24	1147	89.1		80	US-08-475-775C-4	Sequence 4, Appli
25	1140.6	88.6		3	US-07-907-935A-4	Sequence 4, Appli
26	1140.6	88.6		9	US-08-200-724-4	Seguence 4, Appl1
27	224.8	17.5		н	PCT-US01-02579-2	Sequence 2, Appli
58	224.8	17.5		٦	PCT-US97-22629-2	cì.
58	224.8	17.5	2141	-	PCT-US98-01507-2	'n
30	224.8	17.5	2141	7	PCT-US98-03604-2	'n
31	224.8	17.5	2141	00	US-08-475-775A-2	Sequence 2, Appli

7912. Fytoda L/2 (pan / 81981). Other seq. (2012. Fytoda L/2) (pan / 81981). Other seq. (2012. Fytoda L/2) (pan / 81981). Colle seq. (2012. Fytoda L/2) (pan

/cgn2_6/ptodata/2/pna/US6005_COMB.seq /cgn2_6/ptodata/2/pna/US6006_COMB.seq

09 423 997904000000000000000000000000000000000	Control analysis Control ana	07 101 capacago comparing analogo analog
22.4 17.5 24.4 17.5 24.4 18.0 24.0 24.0 27.0 2.2 3.2 3.2 3.2 3.2 3.2 3.2 3.2 3.2 3.2	ALIGNMENTS RESULT 1. 17.9-4 THE CHARLES AL ADJUGUIO 257.9-4 RESULT 2. 17.9-4 RESULT 2. 17.9-4 RESULT 3. 17.9-7 RES	Company Comp

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1201 ggtggttcttcgctgggtattgatgccatgatggccggtgatgccattaacaatatggca 1260
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IN PLANTS
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COMPUTER: IRM PC COMPACTAN
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PERCHILIN RELEASE #1.0, Version #1.30
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STRET: CLINCON Square, P.O. Box 1051
CITY: Rochester
STATE: New YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cornell Research Foundation, Inc
VENTION: ENHANCEMENT OF GROWTH II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US98/01507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application PC/TUS9801507
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy G
COMPUTER: IBM PC COMP
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TITLE OF INVENTION:
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                                                           COMPUTER REMAILED FOUNDER.
RELIGIOR TREEL. PLOSPY clist
COMPUTER: IN THE COMPUTER.
COMPUTER: IN THE COMPUTER.
SOFTWARE: PATCHINE Release #1.0, Version #1.30
ROTHERN FAPLICATION DATA.
APPLICATION WINNER: POT/ISSY/22659
                                                                                                                                                                                                                                                                                                                                                         NAME: CG1 Idam, MC10ac1 L.
REGISTRATION NUMER: 30,727
REGISTRATION NUMER: 30,727
TREMCOMMINICATION INFORMATION:
TREADMONE (176, 263-1304
TREADMA: (716, 263-1304
TREADMA: (716, 263-1304
TREADMA: (716, 263-160)
SUDUMATION FOR SED ID NO. 4;
SUDUMACTERISTICS;
                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,230
APLICATION NUMBER: US 66/033,230
ATTORNEY/AGENT INFORMATION:
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    New York
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                                              14603
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           99ttc9tc9ccgctgggcggcaaagggctgcaaaacctgagcgggccggtggactaccagcag 840
                                                                                          ctccttggcaacggggactgggaggtggtcagggcggtaatgctggcacgggtcttgac 780
                                                                  GGTTCGTCGCTGGCGGCAAAGGGCTGCAAAACCTGAGCGGGCCGGTGGACTACCAGCAG 840
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TITLE OF HAVBHYON: INSECT CONFOC HITLE
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE AUDRESS:
ADDRESSES:
NATOR, Hargrave, Devaus & Doyle LLP
STREET: P.O. Box 1051, Clinton Square
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/03604
                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,226
FILING DATE: 28-FBB-1997
ATTORNEY AGENT THY PROMANTION:
NAME: Goldman, Michael L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application PC/TUS9803604
GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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NEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US98-03604-4
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; Pred. No. 0;
0; Mismatches 0; Indels 0;
       PRICE APPLICATION DATE.

PRICE APPLICATION NUMBER: US 50/036,048
FILING DATE. 27-74N-1997
FILING DATE. 27-74N-1997
NAME: Goldman, Michael L.

RESIGNATION NUMBER: 196091203
REFERENCE/POCKET NUMBER: 1960912502
                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1288; Conservative 0;
                                                                                                    TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     ) TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
pcr-US98-01507-4
                                                                                                                                               LENGTH: 1288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CLASSIFICATION:
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Page 5

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        **PRILCHAFF 12009*** APPLICATE TO A PRILIT TO A PRILITANT BARRY BA
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COMPETER: IN FOCOMPACINE
COMPETER: IN FOCOMPACINE
SOFTMEN FLOCOMPACINE
SOFTMEN FACINITY DELEASE #1.0, Version #1.30
MPLICATION WINGER: US/08/651,376
FLLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Nixon, Hargrave, Devans & Doyle LLF
Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,772
REFERENCE/DOCKET NUMBER: 19603/10035
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/200,724
FILING DATE: 23-FEB-1994
ATTORNEY/AGENT INFORMATION:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (716) 263-1304
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
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U.S.A.
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 14603
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OMPOTER: IM Pr Company Ann
ORPATING SYSTEM: PC-DOS/MN-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: APLICATION DAYA:
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Clinton Square, P.O. Box 1051
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RROLA RPLICATION NUMBER: 08 0/048,109

FILING DARE: 30 AMA-1.93

FULLING DARE: 30 AMA-1.93

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TREATERNA (716) 763-1
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GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.
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STREET: Clinton Square, P.O. Box 1051
CITY, Robester
STATE: New York
ZTATE: New York
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APPLICATION NUMBER: 09/013,587
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**Reprince*** Application US/09770693

**PRILCANT*** Best. Stewen V.

**PRILCANT*** Baser. David W.

**TITLE OF UNFORTION OF OFFICETS**-RESISTANT TRANSERIC PLANTS BY VIPTUB.

**TITLE OF UNFORTION OF THOUSED EXPRESSION OF A HIPPSENLOODED

**TITLE OF INVERTION:** PATHOGRA-INDUCED EX
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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ORGANISM: Erwinia amylovora
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GENERAL INFORMATION:
APPLICANT: Wei, Zhong-Min
APPLICANT: Qiu, Dewen
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Best Local Similarity 100.0%;
Matches 1288; Conservative (
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US-09-835-684-4
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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Pred. No. 0;
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TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
FILE REPERENCE: 19603/2501
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                                           CUBRENT APPLICATION NOMERO, US_09/770,693
CUBRENT APPLICATION NUMBER: 01-26
PRIOR APPLICATION NUMBER: 60/18,565
PRIOR APPLICATION NUMBER: 60/18,565
NUMBER: 07 SEQ ID NOS: 26
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Best Local Similarity 100.
Matches 1288; Conservative
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LENGTH: 1288
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   APPLICANT: Fan, Hao
APPLICANT: Mel, Zhong-Min
TILE OF INVENTION: HYPERSENSITIVE
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                                                                      Sequence 4, Application US/09879248
GENERAL INFORMATION:
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ORGANISM: Erwinia amylovora
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Matches 1288; Conserv
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ES-10-0-129-666/L/C
Sequence 680. Application US/10105399
GERBEAL PRODUCTION:
TITLE OF INVENTION: Use a Secreted Proteins
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GURBEAT PAPLICATION: Use a Secreted Proteins
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Polgo 
                                                                                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-984-827-40
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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us-09-770-693-4.rnpn

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228 cgtcaatcagctggctggcttactcaccggcatgatgatgatgaggatgatgggggg 287
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2.8%; Score 35.4; DB 5; Length 262;
Best Local Similarity 56.8%; Prod. NO. 0.42;
Matches 67; Conservative 0; Mismarches 51; Indels Watches 25; Conservative 0; Mismarches 51; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; OTHER INDOMATION: Incyte ID No: hu00613598
US-09-54-2108-15876
PRIOR FILING DATE: June 9, 1998
PRIOR FILING DATE: June 9, 1998
PRIOR FILING DATE: June 13, 1997
NUMBER OF SEQ ID NOS: 35654
SOFTWARRE: PEEL PROGRAM
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             688 ctgtcgggcctgatggtaatggtctgagccagctccttggcaacgggggactgggaggt 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               748 ggtcagggcggtaatgctggcacggtcttgacggttcgtcgctgggcgaaagggctg 807
                                                                                                                                                                                                                                                                                                                                 Owery Match 2.9%; Score 36.8; DB 6; Length 41205; Best Local Similarity 51.9%; Pered No. 2. Matches 83; Conservative 0; Mismatches 77; Indels 0; Matches 775; In
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Belageane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart Laura L.
                                                                                                                      ORGANISM: Homo sapiens
US-10-105-299-6862
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                     LENGTH: 41206
                                                                           TYPE: DNA
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MERICANET MIT VARIAGE
TITLE REPRESENCE: PI-CALLE MIT VARIAGE
TITLE APPENDENT DOI: SECRETED PROTEINS
THE REPRESENCE: PI-CALLE MINISTER: PI-CALLE MI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 TCGGGAGAGGGAGCAGCACCATCGCAGAGGCATGCCAAGATGCCACAGATGTTGTGAA 368
                                                                                                                                                             Query Match 2.7%; Score 34.4; DB 6; Length 687; Prest Loud. 2.2; Pred. No. 2.2; Pred. No. 2.2; Matches 62; Conservative 0; Mismatches 46; Indels Matches 22; Conservative 0; Mismatches 46; Indels 9
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2.6%; Score 33; DB 1; Length 2600;
Best Local Similarity 50.3%; Pred. No. 8.6; No. 8.6;
Best Conservative (Hismatches 80; Indels
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OTHER INFORMATION: Incyte ID No: 5627037CB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application PC/TUS0209820 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DUGGAN, Brendan N.
ELLIOTT, Vicki S.
FORSTHE, Ian J.
GANDHI, Ameena, R.
GIETZEN, Kimberly, J.
GRIFFIN, Jennifer A.
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LU, Dyung Aina M.
MASON, Patricia M.
SANJAWALA, Madhu M.
SWARNAKAR. Anita
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HONCHELL, Cynthia D.
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TRAN, Uyen K.
WALIA, Narinder K.
WARREN, Bridget A.
YAO, Monique G.
YUE, Henry
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LAL, Preeti G.
LEE, Ernestine A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAUGHN, Mariah R.
BURFORD, Neil
DING, Li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TANG, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US02-09820-33
           US-10-115-123-61
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PETLICANT SELLIMENT, ESTERN J.

PETLICANT SURVE, LEBER L.

PETLICANT SURVEY, SER J.

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10 gggcacctdatggggacagcattggacctgcttcagctactggctaggagtctca 157
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TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029G30APID2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
15 OFFHR INPORMATION: Incyte ID No: hu00160102
10 OFFHR INPORMATION: Incyte ID No: hu00160102
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                                                                                                                                                                                                                                                                  DS-09-539-331D-13185; Sequence 13185, Application US/09539331D; GENERAL INFORMATION:
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GENERAL INFORMATION:
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US-10-115-123-61/c
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LENGTH: 687
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ORGANISM: Homo sapiens

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281 tgggcggtggtggtggtgatgggcggtggcttaggcggtggcttaggtaatggcttgggtg 340
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Pred. No. 9.4;
0; Mismatches 24; Indels 0;
                                                                          Score 32.8; DB 6; Length 507;
Pred. No. 5.4;
                                                                                                                                                                                 0: Mismatches 37: Indels
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TITE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
FILE REFERENCE: FA-0045 US
CHRRHY TAPLICATION NUMBER: 10S/10/116,802
CHRRHY FILING DATE: 2002-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1382961.3
US-10-116-802-138
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APPLICANT: Weng, Gezh
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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PRIOR PELICATION NUMBER: 60/281,593
RIGHER PLILING DATE: 2010-40-40
SOFTWARE: PERL PROGRAM
SEQ IN 00.188
LENGTH: 1645
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GENERAL INFORMATION:
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GENERAL INFORMATION:
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Best Local Similarity 66.2%;
Matches 47; Conservative (
                                                                                             Query Match 2.5%;
Best Local Similarity 59.8%;
Matches 55; Conservative
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Rang, Jian rul
Wang, Jian
Zhou, Ring
Kethman, Tom
Wang, Jian-Rul
Ghosh, Malabika
Zhao, Qing A.
Asundi, Vinod
Ren, Petyand
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                   2152 GGGATGGGAGTTGAACTTCTCATAGTTCTCGTAGGACAGCTGGTTGTTGTCTCAGGCC 2093
                                                                                                                                                                                                                                         2092 AGCTGGGCAGGGCCAGGGGTGGGCTCAGGCCCATAGTCAGAGGCAGGGCCCC 2033
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710 gtctgagccagctccttggcaacgggggactgggaggtggtcagggcggtaatgctggca 769
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THILD OF INVESTIONS IMMAN SECRETE OF PROCESS
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GENERAL INPORMATION:
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GENERAL INFORMATION:
APPLICANT: Hohn, T.
APPLICANT: SAIMSTON, J.
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US-10-105-299-11024
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; ORGANISM: Plasmid US-10-074-279-11

TYPE: DNA

RESULT 8 US-10-105-299-11024

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TYPE: DNA ORGANISM: 1

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TITLE OF CANTAIN LAW, THE SEQUENCE DETERMINED DAM Fragments and COrresponding Polypept 1711.0 G INDEVIOUS Sequence Determined DAM Fragments and COrresponding Polypept CHESCH TO STRONG THE SECURITY SECURITY SEQUENCES TO STRONG THE SECURITY SEQUENCES TO STRONG THE SECURITY SEQUENCES TO STRONG THE SECURITY SECURITY SECURITY SEQUENCES TO STRONG THE SECURITY SECURIT
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Pred. No. 11;
0; Mismatches 59; Indels (
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Job time: 6480 sec
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Best Local Similarity 53.2%;
Matches 67; Conservative
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OTHER INFORMATION: any n =
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OTHER INVATION: Incyte ID No: LI:011822.6:2001MAY17
PCT-USG2-09944-157
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FILE REFERENCE: PT-1231 PCT
CURRENT APPLICATION NUMBER: PCT/USO2/09944
CURRENT FILING DATE: 2002-03-27
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GENERAL INFORMATION:
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ALIGNMENTS

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	T 1 863 AAW75863 Standard;	
	Protein;	
	403 AA	
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Erwinia amylovora hypersensitive response elicitor (HRE). 07-DEC-1998 (first entry) Hypersensitive response elicitor; HRE; insect resistance; biological control; transgenic plant.

Erwinia amylovora.

28-FEB-1997; 97US-0039226. 26-FEB-1998; 03-SEP-1998. W09837752-A1. 98WO-US03604

Wei Z, Zitter TA; (CORR) CORNELL RES FOUND INC

Use of hypersensitive response elicitor polypeptide - for application to plants or seeds or transgenic plants or seeds for the control of insects. WPI; 1998-495374/42. N-PSDB; AAV54607.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 2079; DB 19; Length 403; Best Local Similarity 100.0%; Pred. No. 1.2e-125; Matches 403; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 15-16; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for enhancing plant growth - comprises use of hypersensitive response elicitor polypeptide or protein which may also effect, e.g. increase in plant height or earlier germination seed
361 PMAGDIGNGUQARGAGGSSLGIDAMMAGDAINNMALGKLGAA 403
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                                                                                                                                         GOFMDOYPEVEGKPOYOKGPGOEVKTDDKSWAKALSKPDDDGMTPASMEQENKAKGMIKE
                                                                                                                                                                                             ggkgiqnisgpvGyqqlgnavgtgigmkagiqalndigthrhsstrsfvnkgdramakei
                                                                                                                                                                                                                                GCKGLQNLSGPVDYQQLGXAVGTGIGHRAGIQALNDIGTHRHSGTRSFVNRGDRAVAXEI
                                                                                                                                                                                                                                                                                                          qgsssggkqptegeqnaykkgvtdal8glmgnglsqllgngglggggggnagtgldgssl
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Best Local
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hypersensitive response elicitor polypeptide to seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-332931/29
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ttsttnspldqalginstsqnddstsgtdstsdssdpmgqilkmfseimgslfgdgqdgt 180
                                                                                                                TTSTTNSPLDQALGINSTSQNDDSTSGTDSTSDSSDPMQQLLKMFSEIMQSLFGDGQDGT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       403 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 2079; DB 19; Length 403; 11arity 100.0%; Pred. No. 1.2e-155; Conservative 0; Mismatches 0; Indels 0;
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I MSENTSGLGASTMQLSIGGAGGNNGLLGTSRQNAGLGGNSALGLGGGNQNDTVNQLAGEL

Best Local : Matches 40

Local Similarity

illarity 100.0%; Conservative 0 403 AA

0;

Score 2079; DB 20; Pred. No. 1.2e-155; ; Mismatches 0;

Indels Length 403 0; Gaps 60

0;

403;

Sequence

The present sequence represents a hypermensitive response clicitor process (size of the content of the process of the content of the process of the process

Claim 4; Page 10-II; 94pp; English.

New fragments of an Erwinia hypersensitive response elicitor protein and related DNA - used to impart disease resistance to plants, to

their growth and to control insects

Beer SV,

Laby RJ,

Wei Z;

1999-070210/06.

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(CORR ) CORNELL RES FOUND INC. (EDEN-) EDEN BIOSCIENCE CORP.
                                                                                                                                                                                                                                                                                                                                              Hypersensitive response elicitor protein; hairpin protein; disease resistance; seed quality; insect control; corn borer;
                                                                                                                                                                                                                                                                                                                                                                         A hypersensitive response elicitor protein
                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                              AAW87639;
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                                                                                                                                                                                                                                                                                                                    Erwinia amylovora.
                                                                                                                                                                                                                                                                                                                                     Lepidoptera larvae; transgenic plant.
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                                                               The parent discloses a method to impart stress resistance to plants by applying a hypersensitive response elicitor in a non-infectious form to applying a hypersensitive response a hypersensitive response a hypersensitive response elicitor protein from Evihia mayora. It is is used to impart stress resistance to plants.
                                                                                                                                               Disclosure; Page 7-8; 84pp; English.
                                                                                                                                                                                     Application of a hypersensitive response elicitor protein to plants
                                                                                                                                                                                                                                 WPI; 2000-376566/32
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Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 403; Conservative 0
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Pred. No. 1.2e-155;
0; Mismatches 0; Indels 0;
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                                               | The state of the
                                                                                                                                                                               403 AA
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Erwinia amylovora hypersensitive response elicitor protein
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Hypersensitive Erwinia amylovora response elicitor; comycete; loss; antifungal transgenic plant; injection

26-JAN-2001; 2001WO-US02579

26-JAN-2000; 2000US-0178565

FOUND INC

Bauer DW;

New chimeric gene, useful for controlling plant-pathogenic fungi and producing comprese-registant transgenic plants, comprises first DNA encoding hypersensitive response elicitor, promoter and regulatory region .

Claim 9; Page 13-14; 72pp; English

The impaction relates to a chiments gone that includes a first DNA contents enough a hypersensitive response childron processor of polypeptide, premoter operably linked 5 to the first DNA molecule of the first polypersens of the first polypersens of the first DNA molecule. The invention also relates to the treat DNA molecule. The invention also relates to transaction plant resistant to distance resultant of monoports of the promoter induces transcription of the first DNA molecule. The promoter induces transcription of the first DNA molecule in the promoter induces transcription of the first DNA molecule. The promoter induces transcription of the first DNA molecule in the promoter induces transcription of the first DNA molecule in the plant DNA molecule in the pl

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Query Match 100.0%; Score 2079; DB 22; Best Local Similarity 100.0%; Pred. No. 1.2e-155; Matches 403; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                      Query Match
Best Local S
Matches 372
                                                                                                                                                                                                                                                                                                                                                                                                   Mila sequesce represents a hypersensitive response elicitor from that sequesce represents the response of the first and the sequence of the sequence
                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Imparting pathogen resistance to plants - with hypersensitive 
response elicitor polypeptide or protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         r'esponse
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tgm#mmmsmmgggtlmggglggglgnglggsgglgeglsnalndmlggslntlgskggnn
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Conservative (
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; Pred. No. 8.6e-144;
0; Mismatches 0;
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     385 AA
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372
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The httpl gene was isolated from & amylowore using a 48-fold degenerate oligonuclectieg probe corresponding to make on acids 9-13 degenerate oligonuclectieg probe corresponding to make the k-remminus of harpin. The 44kD protein encoded by the httpl gene is a hypersensitive response elicitor protein. The harpin is thought to be an archetype for ms elicitors from phytopathogenic thought.
                                                                                                                                                                                                                                                                       Hypersensitive response elicitor protein derived from Erwinia
amylovora - and DNA mocoding it. useful for developing barpin
inhibitors to prevent e.g. fire blight of fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harpin, hypersensitive response elicitor; HR-elicitor; itre blight nosaceae; apple, pear; phytopathogenic batteria; defence reaction; hypersensitive reaction and pathogenicity; hrpN; gene cluster; ds.
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Best Local s
Matches 369
This sequence represents a hypersensitive response elicitor from Ervinia chrysanthemi, with a mol. Nr. of 34,000. The elicitor is thermostable, has a glycine content of over 16%, and has no cysteine.
                                                                                                                                                                                                                                                                                W09639802-A1
                                                                                                                                                                                                                                                                                                                              Hypersensitive response, elicitor, Erwinia chrysanthemi; plant; disease-resitance; Escherichia coli; infiltration; virus; bacterium; fungus; pathogen; biological control agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW06597 standard; Protein; 338 AA.
                                                                        Imparting pathogen resistance to plants - with hypersensitive 
response elicitor polypeptide or protein
                                                                                                                                                      Beer SV,
                                                                                                                                                                             (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                              05-JUN-1996;
                                                                                                                                                                                                                                                        19-DEC-1996
                                                                                                                                                                                                                                                                                                       Erwinia chrysanthemi.
                                                                                                                                                                                                                                                                                                                                                                                  Hypersensitive response elicitor protein
                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW06597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.0%;
Local Similarity 99.5%;
hes 369; Conservatur-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                               1997-051614/05
DB; AAT49313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pmagdtgngn1 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PMAGDIGNGNL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gqfmdgypevfgkpqyqkgpgqevktddkswakalskpdddgmtpasmeqfnkakgmikr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSLNTSGLGASTMQISIGGAGGNNGLLGTSRQNAGLGGNSALGLGGGNQNDTVNQLAGLL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQFNDQYPEVFGKPQYQKGPGQEVKTDDKSWAKALSKPDDDGMTPASMEQFNKAKGMIKR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggkglrglsgpvdygglgnavgtgigmkagigalndigthrhsstrsfvnkgdramakei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGKGLQNLSGPVDVQQLGNAVGTGIGMKAGIQALNDIGTHRHSSTRSFVNKGDRAMAKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGSSSGGKQPTEGEQNAYKKGVTDALSGLMGNGLSQLLGNGGLGGGQGGNAGTGLDGSSL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttsttnspldgalginstsgnddstsgtdstsdssdpmgqllkmfseimgslfgdgdgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTSTTNSPLDQALGINSTSQNDDSTSGTDSTSDSSDPMQQLLKMFSEIMQSLFGDGQDGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGMMMMSMMGGGGLMGGGLGGGLGNGLGGSGGLGEGLSNALNDMLGGSLNTLGSKGGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 msintsgigastmqisiggaggnngligtsrqnagliggnsalgliggnqndtvnqlagli 60
                                                   Page
                                                 44; 69pp; English.
                                                                                                                                                                                                     95US-0475775.
                                                                                                                                                                                                                              96WO-US08819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1913; DB 15;
Pred. No. 1.3e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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300 LGOPNDOYDEVFGKPOYOXGPGQEVKTDDXSWAKALSKPDDDGMTPASMEQFNKAKGNIK 359

iggfmdgypeifgkpeyqkdgwsspktddkswakalskpdddgmtgasmdkfrgamgmik

235

AAW87638

09-MAR-1999

(first entry)

AAW87638;

AAW87638 standard; Protein; 338 AA

28-MAY-1998; 03-DEC-1998 W09854214-AZ Erwinia chrysanthemi.

30-MAY-1997;

97US-0048109 98WO-US10874

(EDEN-) EDEN BIOSCIENCE CORP.

Hypersensitive response elicitor protein; hairpin disease resistance; seed quality; insect control; Lepidoptera larvae; transgenic plant.

COLU DOLEL

A hypersensitive response elicitor protein.

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Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 MQISI-GGAGGNNGLLGTSRQNAGLGG-NSA---LGLGGGNQNDTVNQLAGLLTGMMMM 67
lgagglgglsgagafnglgnaigmgvgqnaalsalsnvsthvdgnnrhfvdkedrgmake
                                                                                                                       LGGKGLQNLSGPVDYQQLGNAVGTGIGNKAGIQALNDIGTHRHSSTRSFVNKGDRAMAKE 295
                                                                                                                                                                                                                                              lansminasqmtqgnmnafgsgvnnalssilgnglgqsm-----sgfsqps
                                                                                                                                                                                                                                                                                                                                                         TQGSSSGGKQPTEGEQNAYKKGYTDALSGLMGNGLSQLLGNGGLGGGQGGNAGTGLDGSS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLDQALGINSTSQNDDSTSGTDSTSDSSDPMQQLLKMFSEIMQSLFG------DGQDG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----fggalagglgas-skglgmsnqlgqsfgn----gaqgasnllsvpk- 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMMGGGGLWGGGLGGGLGGGGGGGGGGLSNALNDMLGGSLNTLGSKGGNNTTSTTNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mqitikahiggdlgvsglgaq--glkglnsaasslgssvdklsstidkltsaltsmm---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -sggdals-----kmfdkalddllghdtvtkltnqsnq 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 718.5; DB
Pred. No. 8.8e-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 18; Length 338
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RESULT 12
AAW82407
ID AAW824
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Best Local Similarity 42.8%; Pred, No. 8. Be-d9;
Matches 173; Conservative 41; Mismatches 111; Indels 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a hypersensitive response slicitor process (also called helpin process) that is able to called to process the process of the
                                                                                                                                                                                                                                   23-FEB-1999
                                                                                                                                                                                                                                                                                                                                               AAW82407 standard; Protein; 338 AA
                       Erwinia chrysanthemi
                                                                             Hypersensitive response elicitor protein; hrpN-Ech; pathogen resistance; plant; transformation; pathogen-inducible promoter.
                                                                                                                                                                 E. CHrysdninemi Hrpw-ECH procein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fragments of an Erwinia hypersensitive response elicitor protein and related DNA - used to impart disease resistance to plants, to increase their growth and to control insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beer SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 savagdtgntnlnlrgaggaslgidaavvgdkianmslgklana 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 RPMAGDYGNONLQARGAGGSSLGIDAMMAGDAINNNALGKLGAA 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 igqfmdqypeifgkpeyqkdgwsspktddkswakalskpdddgmtgasmdkfrqamgmik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGGKGLQNLSGPVDYQQLGNAVGTGIGHKAGIQALNDIGTHRHSSTRSFVNKGDRAMAKE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lansmlnasqmtqgnmnafgsgvnnalssilgnglgqsm-----sgfsqps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TQGSSSGGKQPTEGEQNAYKKGVTDALSGLMGNGLSQLLGNGGLGGGQGGNAGTGLDGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLDQALGINSTSQNDDSTSGTDSTSDSSDPWQQLLKMPSEIMQSLPG-------DGQDG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999-070210/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGQFMDQYPEVFGRPQYQXGPGQEVRTDDXSWAKALSKPDDDGMTPASMEQFNKAKGMIK 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rgaggrqg1sgagarnq1gna1gmgvgqnaa1sa1snVsEnVdgnnrnIvdkedrgmake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----sggdals-----kmfdkalddllghdtvtkltngsng 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMMGGGGLMGGGLGGGLGGGGLGEGLSNALNDMLGGSLNTLGSKGGNNTTSTTNS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mqitikahiggdlgvsglgaq--glkglnsaasslgssvdklsstidkltsaltsmm---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MQISI-GGAGGNNGLLGTSRQNAGLGG-NSA---LGLGGGNQNDTVNQLAGLLTGMMMM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laby RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 AA;
                                                                                                                                                                                                                             (Tirst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wei
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08-SEP-2000

(rirst entry)

AAY71092 standard; Protein; 338 AA

L

Hypersensitive response elicitor; environmental stress plant.

resistance

Erwinia chrysanthemi hypersensitive response elicitor

9 Db Ş Db Š Db Ş 5 S Db Ş Db

235 300

1gqfmdqypeifgkpeyqkdgwsspktddkswakalskpdddgmtgasmdktrqamgmik IGQFMDQYPEVFGKPQYQKGPGQEVKTDDKSWAKALSKPDDDGMTPASMEQFNKAKGMIK 359

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Query Match
Best Local S
Matches 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a novel Erwinia chrysanthemi proctain, hrpk-reb, that elicits a hypersensitive response in plants. The encoding DNA can be used for imparting pathogen resistance to plants, by transforming a plant with a weetor containing the DNA and a pathogen-inducible promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Column 29-30; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding Erwinia chrysanthemi hypersensitive response proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI: 1999-069852/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bauer D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
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175
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                                                                                                                                                                                                                                                                                 128 PLDQALGINSTSQNDDSTSGTDSTSDSSDFMQQLLKMFSEIMQSLFG------DGQDG 179
                                                                                                                                                                                                                                                                                                                                     56
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                            LGGKGLQNLSGPYDYQQLGNAVGTGIGMKAGIQALNDIGTHRHSSTRSFYNKGDRAMAKE 299
lgagglqglsgagainqlgnaigmgvgqnaalsalsnvsthvdgnnrhivdkedrgmake
                                                                                                            Lansminasqmtqgnmnafgsgvnnaissiigngigqsm-----sgisqps
                                                                                                                                                               TQGSSSGGKQPTEGEQNAYKKGVTDALSGLMGNGLSQLLGNGGLGGGQGGNAGTGLDGSS 239
                                                                                                                                                                                                                                                                                                                                     -----fggalaqglgas-skglgmsnqlgqsfgn----gaqgasnllsvpk- 96
                                                                                                                                                                                                                                                                                                                                                                                              SMMGGGGLMGGGLGGGLGMGLGGSGGLGEGLSNALNDMLGGSLNTLGSKGGNNTTSTTNS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MQISI-GGAGGNUGLLGTSRQNAGLGG-NSA---LGLLGGGNQNDTYNQLAGLLTGMMAMM 67
                                                                                                                                                                                                                        -----sggdals-----kmfdkalddllghdtvtkltngsng 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV73494, AAV73507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collmer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0484358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0484358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.6%; Score 718.5; DB 20; Length 338
42.8%; Pred. No. 8.8e-49;
tive 41; Mismatches III; Indels 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             indels 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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AAY84853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.6%;
Best Local Similarity 42.8%;
Matches 173; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The patent discloses a method to impart stress resistance to plants by applying a hypersensitive response elicitor in a non-infectious form to a plant or seed. The present sequence is a hypersensitive response elicitor protein from brainia chrysanthemi. The protein is heat stable and used to impart stress resistance to plants.
                            AAT84853 standard; Protein; 338 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 4-5; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application of a hypersensitive response elicitor protein to plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAD00667
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                                                                                                                                                                                                                                                                                    235
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                                                                                                                                                                 295 savagdtgntnlnlrgaggaslgidaavvgdkianmslgklana
                                                                                                                                                                                              360 RPMAGDTGNGNLQARGAGGSSLGIDAMMAGDAINNMALGKLGAA 403
                                                                                                                                                                                                                                                                                                                                                                                            175 lgagglqglsgagafnqlgnaigmgvgqnaalsalsnvsthvdgnnrhfvdkedrgmake
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 MQISI-GGAGGNNGLLGTSRONAGLIGG-NSA---LGLGGGNONDTVNQLAGLLTGMMMM 67
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                                                                                                                                                                                                                                                                                                           IGQFWDQYPEVFGKFQYQKGFGQEVKTDDKSWAKALSKPDDDGWTPASMEQFNKAKGMIK 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGGKGLQNLSGPVDYQQLGNAVGTGIGMKAGIQALNDIGTHRHSSTRSFVNKGDRAMAKE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----sggdals------kmfdkalddllghdtvtkltnqsnq 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ); Score 718.5; DB 21;
b; Pred. No. 8.8e-49;
41; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 338;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or the present sequence represents a hypersonative response elicitor of physpeties. The sportfest of dearthly shypersonative response of elicitor polypopide fragents, which do not elicit a hypersonative calcitor polypopide fragents, and the control insects in the polypopide state of the control insects in the polypopide control insects in the polypopide state of the control insects in the polypopide control insects in the polypopide control in the control insects in the polypopide control insects in the polypopide control insects and the control insects of the polypopide control insects and the control insects in the polypopide control insects and the control insects in the control insects and the control insects in the control insects and 
                                                                                                                                                                                                                                                                                                                                                                                            Matches 1/3;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 6-7; 100pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypersensitive response elicitor polypeptides useful for imparting enhanced growth, disease resistance and insect resistance to plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                petunia, pelargonium, poinsettia, chrysanthemum, carnation or zinnia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wei Z, Fan H, Niggemeyer JL
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                                                                                                             128 PLDQALGINSTSQNDDSTSGTDSTSDSSDPMQQLLKMFSEIMQSLFG------DGQDG 179
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                                                                                                                                                                                                                           68 SMMGGGGLMGGGLGGGGLGNGLGGSGGLGEGLSNALNDMLGGSLNTLGSKGGNWTTSTTNS 12
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                                                                                                                                                                       -----fggalagglgas-skglgmsnqlgqsfgn----gaqgasnllsvpk-
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180 TQGSSSGKQPTEGEQNAYKKGVTDALSGLMGNGLSQLLGNGGLGGGQGGNAGTGLDGSS 239

-sggdals-----kmfdkalddllghdtvtkltngsng 128

96

338 AA; Conservative

42.8%;

41; Mismatches 111; Indels 79; Score 718.5; DB 21; Length 338; Pred. No. 8.8e-49;

sdps

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05-OCT-1998;
                                             05-OCT-1999;
                                                                                                                                                                                                                                                                                                          ornamental plant.
                                                                                                                                                                                                                                                                                                                                 Hypersensitive response; insect control; disease resistance; hypersensitive response elicitor; plant growth; vegetable; crop;
                                                                                                                                                                                                                                                                                                                                                                                                     A hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                              08-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY84853;
                                                                                          13-APR-2000
                                                                                                                                   WO200020452-A2
                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                  Erwinia chrysanthemi.
9808-0103050
                                             99WO-US23181
                                                                                                                                                                                                  Location/Qualifiers
20
                                                                                                                                                                            /note= "encoded by CTGGGTGCT"
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	SMAGGGGLMGGGLGGGLGNGLGGGGLGBGLSNALNDMLGGSLNTLGSKGGNNTTSTTUS	Q I
1000M 67	13 MOIST-GGAGGNNGLLGTSRQNAGLGG-NSALGLGGGNQNDTVNQLAGLLTGMMANAM 67	B 5
Gaps	Query Match 34.6%; Score 718.5; DB 21; Length 338; Best Local Similarity 42.8%; Pred. No. 8.8c-49; Matches 173; Conservative 41; Mismatches 111; Indels 79;	* 8 0
	Sequence 338 AA:	SO
-	ensitive response elicitor protein HrpN	188
pectar nt of	tyase. E. chrysanthemi is a pathogen involved in the development of	88
themi, a	it acts as an antigen). The protein is derived from E. chrysanthemi, a bacteria with a wide host range which rapidly kills and macerates host	88
othemi, may be	The invention provides a protein (HrpNECH) from Erwinia chrysanthemi, which elicits a hypersensitive response in plants. The protein may be used to produce hypersensitive responses to pathogens in plants (1.e.	888
	Claim 1; Fig 1; 26pp; English.	X S
ve	Isolated Erwinia chrysanthemi useful for eliciting hypersensitive responses in plants $\mbox{\ensuremath{^{\circ}}}$	EES
	WPI; 2000-061904/05. N-PSDB: AAZ39563, AAZ39567.	X 72 72
	Collmer A, Bauer D;	22
	(CORR) CORNELL RES FOUND INC.	X P S
	07-JUN-1995; 95US-0484358.	¥ # 3
	17-JUL-1998; 98US-0118959.	F F
	14-DEC-1999.	383
	US6001959-A.	P
	Erwinia chrysanthemi.	\$ 8 £
	Hypersensitive response elicitor; pathogen; antigen; bacteria; macerating enzyme; pectate lyase; soft rot; HrpNECH.	22
	E. chrysanthemi hypersensitive response elicitor protein.	X E S
	28-FEB-2000 (first entry)	333
	AAY55801;	18
	RESULT 15 ANT5501 XV ANT55801 standard; Protein; 338 AA.	AAY S
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58 SMMGGGGLMGGGLGGGLGGGGGGGGGGLGEGLSNALNDMLGGSLNTLGSKGGNNTTSTTNS 127

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        129 lansmlnasgmtqgrmnafgsgvnnalssllgngllgqsm-----sgfsqps
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Search completed: May 2, 2002, 03:32:12 Job time: 648 sec



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Listing first 45 summaries
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Maximum DB seg length: 2000000000
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Perfect score:
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some greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Patent No. 5849868
      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 403; Conservative
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APPLICANT: Beer, Steven V.
APPLICANT: Beer, Steven V.
APPLICANT: Callmer, Alan
APPLICANT: He, Sheng-Yang
APPLICANT: LABAP, Non J.
TITHLE OF INVENTION: IP JAMES
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
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STREET: Clinton:
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
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ZIP: 146
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                         NAME: GOLdman, Michael L.

BEGISTRATION MIMBER: 90,727

BETERBAYE, DOCKET MIMBER: 1966

FELEOMANICATION, HYDRAMFION,

FELEPHAN: (176), 263-1304

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Patent No. 5977060
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APPLICANT: Wei, Zhony-Min
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
TOPOLOGY: linear
MOLECULE TYPE: protein
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STREET: P.O., Box 1051, Clinton Square
CITY: Rochester
STATE: New YORK
COUNTRY: U S.A.
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US-08-851-376A-2
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Patent No. 6174717
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                                                                                                                                                                                                                                                                                                                                 ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/200,724
FILING DATE: 3-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                      COMPUTE: IDM PC compatible
OPERATING SYSTEM: PC-005/MS-TOS
SOFFWARE: Patentin Release 41.0, Version #1.30
CURBENT APPLICATION DATA:
APPLICATION MOMERE: US/06/851.376A
PILING DATE: 05-WAY-1957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wei, Zhong-Min
APPLICANT: Bauer, David W.
APPLICANT: Collmer, Alan
APPLICANT: He, Sheng-Yang
APPLICANT: Laby, Ron
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Nixon
STREET: Clinton
CITY: Rochester
STATE: NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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141 GCKGLONLSGPVDYOLGANVGTGIGKKAGIQALNDIGTHRISSTRSFVKKGDRAMAKEI 300
241 GCKGLONLSGPVDYOQLGNAVGTGIGKKAGIQALNDIGTHRISSTRSFVKKGDRAMAKEI 300
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121 TTSTTMSPLDQALGINSTSQNDDSTSGTDSTBDSGDWQQLLKWFSEINGSLFGDQQCGT 180
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REGISTRATION NUMBER: 30
REFERENCE/DOCKET NUMBER:
                                                    NAME: Goldman, Michael
                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TGMMMSMMGGGGLMGGGLGGGLGNGLGGGSGGLGEGLSNALNDMLGGSLNTLGSKGGNN 120
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1 MSIATSGLGASTWOISIGGAGGNWGLLGTSRONAGLGGNSALGLGGGWONDTVANGLAGLL 60
1 MSIATSGLGASTWOISIGGAGGNNGLLGTSRONAGLGGNSALGLGGGWONDTVANGLAGLL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clinton Square, P.O. Box 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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US-08-851-376A-2
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Best Local Similarity 100.0%;
Matches 403, Conservative C
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TELEPHONE: (716) 263-1304
TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                            MPPLICANT: 041, Devon
APPLICANT: 041, Zhong-Min
TITILE 0F INVENTION: RESISTANCE IN PLANTS BY SEED TREATHENT
TITILE 0F INVENTION: RESISTANCE IN PLANTS BY SEED TREATHENT
                           COMPUTER REMONALE PODE:
MEDIUM TYPE: 120ppY disk
COMPUTER: IRM PC compatible
OPERATINE SYSTEM: PC-DS/MS-DOS
OPERATINE SYSTEM: PC-DS/MS-DOS
OPERATE APPLICATION DAVIS: 0404 A07
URBERT APPLICATION DAVIS: 0404 A07
                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 PMAGDTGWGNLOARGAGGSSLGIDAMMAGDAINNALGKIJAA 403
361 PMAGDTGWGNLOARGAGGSSLGIDAMMAGDAINNALGKIJAA 403
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             APPLICATION NUMBER:
                                                                                                                                                 COUNTRY
                                                                                                                                                                                       CITY: Rochester
                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                          ADDRESSEE:
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FILING DATE:
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                                                                                                                                   14603
                                                                                                                                                 New York
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                                                                                                                                                                                                     E: Nixon, Hargrave, Devans & Doyle LL
P.O. Box 1051, Clinton Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linear
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                 US/08/984, 207
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Pred. No. 5.8e-175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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                                                                                         CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                         SIP:
                                                       COUNTRY:
                                                                        STATE:
                                                                                                                         ADDRESSEE:
                                         14603
                                                          U.S.A.
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CLASSIFICATION

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Sequence 3, Application US/09013587
Patent No. 6277814
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
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REFERENCE/DOCKET NUMBER: 19603/1201
TELECOMMUNICATION INFORMATION:
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LENGTH: 403 amino acids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS
                                                                                                                                                                                                                                                                                       APPLICANT: Qiu, Dewen
APPLICANT: Wei, Zhong-Min
APPLICANT: Beer, Steven V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TESTINSPLOALGINSTSONDOFFSCTDSTSDSSDPMQCLLXMSSEIMGLEGOGOGOT
121 TESTINSPLOALGINSTSONDDSTSGTDSTSDSSDPMQCLLXMSSEIMGSLEGOGOGOT
121 TESTINSPLOALGINSTSONDDSTSGTDSTSDSSDPMQCLLXMSSEIMGSLEGOGOGOT
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TELEFAX: (716) 263-1600
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                                                                                                                     New York
                                                                                                                                                                 3: Nixon, Hargrave, Devans & Doyle LLP
Clinton Square, P.O. Box 1051
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REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 1960
TELEOMANINCATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1304
INFORMATION FOR SEQ ID NO: 33
                                                                                                                                                                                          Sequence 3, Application US/08891254
Patent No. 5776889
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                                                                                                                                                                           GENERAL INFORMATION
                                                   APPLICANT: Wel, Zhong-Min
APPLICANT: Mear, Steven V.
TITIES OF INVENTION: Hypersensitive Response
TITIES OF INVENTION: Induced Resistance in Plants
NUMBER OF SDOUBNESS:
CRESSPONDANCE ADDRESS:
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FILLING DATE: 27-JAN-1997
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: PS-tentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,587
FILING DATE:
FILING DATE:
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LENGTH: 403 amino acid
TYPE: amino acid
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               STREET:
                                   ADDRESSEE:
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MSLATSGLGASTMOISIGGAGGNWGLLGTSRONAGLGGNSALGLGGGNQNUTVPAGLAGIL 60
MSLATSGLGASTMOISIGGAGGNWGLLGTSRONAGLGGNSALGLGGGNQNUTVAQLAGIL 60
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Similarity 100.0%;
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amino acid
               E: Nixon, Hargrave, Devans & Doyle
Clinton Square, P.O. Box 1051
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Pred. No. 5.8e-175;
D; Mismatches 0;
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TITLE OF INVENTION:
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BODISTRATION HYDRE: 30.727
REFERENCE POORTE HYDREE: 1466
REFERENCE POORTE HYDREE: 1466
REFERENCE POORTE POO
                                                                                                                                                                                          ; Sequence 3, Application US/08819539
; Patent No. 5859324
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Best Local Similarity 100.0%; Pred. No. 1e-161;
                                       GENERAL INFORMATION:
APPLICANT: Wei, Zhong-Min
APPLICANT: Beer, Steven V
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APPLICATION WHORE: 10-UU-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION MURMER: 08/475.775
APPLICATION MURMER: 08/475.775
APPLICATION MURMER: 08/475.775
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COUNTRY: U.S.A.
ZIF: 14603
ZIF: 14603
COMPUTER READALE POWE:
COMPUTER READALE POWE:
COMPUTER: THE PCOMPATIBLE
RECOMPUTER: THE PCOMPATIBLE
OPERATION SISTEM: UP-DOS/MS-DOS
SOFWARE: Detect in Release #1.0, Version #1.30
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Hypersensitive Response
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US-08-819-539-3
PCT-US96-08819-
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Best Local Similarity 100.0%; Pred. No. 1e-151;
Matches 372; Conservative 0; Mismatches 0; Indels
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LEWSTH: 385 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING STSTEM: PC-DOS/NS-DOS
SOFTWANE: Patent In Release #1.0, Version #1.30
CHRENDY APPLICATION MONTH:
APPLICATION MONES: US/06/819.539
FILING DATE: 137-MAR-1997
CLASSIFICATION MONTH: 800
PRICON APPLICATION MONTH: A
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: IN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (716) 263-1304
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                                                                                      361
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REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 14603/10050
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CITY: Rochester
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                                                                                      PMAGDTGNGNLQ 372
                                                                                                                                    PMAGDTGNGNLQ 372
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Clinton Square, P.O. Box 1051
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GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 18-161;
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TELEPHONE: (716) 263-1304
TELEPHAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 maino acids
TELEPHAX: 185 maino acids
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ATTORNEY/ADENT INFORMATION:
NAME: GGIdman, Michael L.
REGISTRATION NUMBER: 30.727
REFERENCE/DOCKET NUMBER: 19603/10051
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: RESISTANCE IN PLANTS
TITLE OF INVENTION: RESISTANCE IN PLANTS
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361
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STRANDEDNESS:
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PMAGD7GNGNLQ 372
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Clinton Square, P.O. Box 1051
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TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACCERTSTICS:
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Best Local Similarity 99.5%;
Matches 369; Conservative
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GENERAL INFORMATION:
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FILING DATE: 01-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,8
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APPLICANT: Bear, Alan Collmer, Sheng-Yang He, and Ron J. Laby
TITLE OF INVENTION: Elicitor of the Hypersensitive Response in Plants
EMMARS OF SEQUENCES: 5
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APPLICATION NUMBER: PC
FILING DATE: 19930630
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301 GORMOOYPEVFGKFOYOKGFGGEWETDDKSMAALJSKPDDDGMTFASMEGPRIAKGHIKR 360
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OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TGMM049KSMAGGGELAGGGELGGGELGGGELGGSGSGELGESELSNALNDMEGGSELTELGSKGGNN 120
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TYPE: amino acid
STRANDEDNESS: single
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CITY: Trumbull
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STREET: 25 Skytop Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1913; DB 5; Length 385;
Pred. No. 2.1e-160;
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US-08-891-254-1
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                                                                            129 LANSMINASQMTQGNMNAFGSGVNNALSSILGNGLGQSM-----SGFSQPS 174
240 LGGKGLQNLSGPVDYQQLGNAVGTGIGMKAGIQALNDIGTHRHSSTRSEVNKGDRAMAKE 29
                                                                                                                                                        180 TQGSSSGGKQPTEGEQNAYKKGVTDALSGLMGNGLSQLLGNGGLGGGQGGNAGTGLDGSS 23
                                                                                                                                                                                                                                                                                                 128 PLDQALGINSTSQNDDSTSGTDSTSDSSDPMQQLLKMPSEIMQSLFG------DGQDG 179
                                                                                                                                                                                                                                                                                                                                                                             56 ------FGGALAQGLGAS-SKGLGMSNQLGQSFGN-----GAQGASNLLSVPK- 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 SMMGGGGLMGGGLGNGLGGSGGLGBGLSNALNDNLGGSLNTLGSKGGNNTTSTTNS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MQITIKAHIGGDLGVSGLGAQ--GLKGLNSAASSLGSSVDKLSSTIDKLTSALTSMM--- 55
                                                                                                                                                                                                                     -----SGGDALS------KMFDKALDDLLGHDTVTKLTNQSNQ 128
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US-08-891-254-1
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                                                                                 Ouery Match 34.6%; Score 718.5; DB 1; Length 338; Best Local Similarity 42.8%; Pred: Nb, 1.5e-15; Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps
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Patent No. 5776889
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Hypersensitive Response
TITLE OF INVENTION: Induced Resistance In Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wei,
APPLICANT: Beer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 14
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COUNTRY: U.S.A.
ZIP: 14603
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CITY: Rochester
STATE: New York
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13 MQISI-GGAGGNNGLLGTSRQNAGLGG-NSA---LGLGGGNQNDTVNQLAGLLTGMMMM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
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FILING DATE: 10-JU
CLASSIFICATION: 51

    Application US/08891254
    5776889

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N: 514
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175 LGAGGLQGLSGAGAFNQLGNAIGMGVGQNAALSALSNVSTHVDGNNRHFVDKEDRGMAKE 234

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	180 TQGSSSGGKQPTEGEQNAYKKGVTDALSGLMGNGLSQLLGMGGLGGGQGGNAGTGLDGSS 239	Ø
	97	망
	128 PLDQALGINSTSQNDDSTSGTDSTSDSSDPMQQLLKMFSEIMQSLFGDGQDG 179	8
	56	몽
	68 SMMGGGGLMGGGLGGGLGGGLGGGGGGGGGGGGGGGGGG	Ę.
	13 MOIST-GGAGGMKILGTSRORANGLGG-NSALGLGGGARDNTVROLAGLITORRORA 67 11 H1: 1	8 8
Į,	Query Match 94.6%; Score 718.55, DB 2; Length 338; Best Local Similarity 42.6%; Prod No. 1.5e-52; Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps	
	PE	g
	STRANDEDNESS: single TOPOLOGY: linear	
	LENGTH: 338 amino acids	
	INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:	٠, ٠,
	TELEFAX: 716-263-1600	
	TELECOMMUNICATION INFORMATION:	
	REFERENCE/DOCKET NUMBER: 19603/840	
	NAME: Goldman, Michael L.	٠
	CLASSIFICATION: 800	
	APPLICATION NUMBER: US/08/484,358 FILING DATE:	
	3,	٠, ,
	8-DOS	
	MEDIUM TERE: KLOPPY GISK COMPUTER: IBM PC compatible	٠. ٠.
	ER READABLE FORM	
	ZIP: 14603	
	Nev	٠
		.,
	ADDRESSEE: Nixon, Hargrave, Devans & Doyle	٠. ،
	SEQUENCES:	
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	OF INVENTION:	
	CANT: Collmer,	٠. ٠
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	295 SAVAGDTGNTNLHLRGAGGASLGIDAAVVGDKTANNSLGKLANA 338	밁
	360	Q
	235 IGQFMDQTPEIFGKPEYQKDGWSSPKTDDKSWAKALSKPDDDGMTGASMDKFRQAMGMIK 294	몽
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Ouery Match 25milarity 42.8%; Score 718.5; DB 2; Length 338; Best Local Similarity 42.8%; Pred. No. 1.5e-55; Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-819-539-1
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Patent No. 5859324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Wei, Zhong-Min
APPLICANT: Beer, Steven V.
                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids
TYPE: amino acid
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ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,775
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Hypersensitive Response TITLE OF INVENTION: Induced Resistance In Plants NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 SAVAGDTGNTHLNLRGAGGASLGIDAAVVGDKIANNSLGKLANA 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 IGQFMDQYPEVFGKPQYQKGPGQEVKTDDKSWAKALSKPDDDGMTPASMEQFNKAKGMIK 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 14603/10050
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CITY: Rochester
STATE: New York
                                                                  STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14603
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-030-270A-1
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                                                                                        Overy Match 34.6%; Score 718.5; DB 2; Length 338; Best Local Similarity 42.8%; pred. No. 1.5e-25; Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps
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Patent No. 5977060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSITIONION 514
PRIOR APPLICATION MAYN:
APPLICATION MANNER:
DE 60/033,226
APPLICATION MANNER:
DE 700-030
APPLICATION
APPLICAT
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INFORMATION FOR SEQ
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MEDITH TYPE: Floppy disk
COMPTER: IBM FO COMPALIA
COMPTER: IBM FO COMPALIA
COMPTER: IBM FO COMPALIA
COMPATING SYSTEM: P-TOSE/MS-DOS
SOFTMARE: Patentin Recesse #1.0, Version #1.30
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APPLICANT: Wei, Zhong-Min
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
TYPES OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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13 MQISI-GGAGGNNGELGTSRQNAGLGG-NSA---LGLGGGNQNDTVNQLAGLLTGMMMM 67
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CITY: Rochester
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STREET: P.O. Box 1051, Clinton Square
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DS-09-TIR-959-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09118959
Patent No. 6001959
         TENOTH: 338 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                          TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: IMM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFMARE: Fatentin Release #1.0, Version #1.30
UUREDY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bauer, David
APPLICANT: Coller, Alan
TITLE OF INVENTION: Mypersensitive Response Elicitor From
TITLE OF INVENTION: Ervinia Chrysanthemi
                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
                                                                                                                                                                                                                                                                                                       NAME: Goldman, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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361 RPMAGDYGNGNLQARGAGGSSLGIDAMAGDAINHAALGKLGAA 403
295 SAVAGDYGNYINLALRGAGGASLGIDAAVVGDKIANMASLGKLANA 338
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                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                      NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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Clinton Square
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Query Match Best Local Similarity

42.8%;

Score 718.5; DB 3; Length 338; Pred. No. 1.5e-55;

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us-09-770-693-3.rai

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Search completed: May 2, 2002, 03:32:44 Job time: 344 sec

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harpin - Bewiila a happin - Bewi	Description	wance to have a suit being printed, pribution.	-			219241			AINNMALGKIGAA 403	.19 Seconds Lignments) illion cell updates/sec		<u>.</u>
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Оу 388	68 SMHGGGGLMGGGLGNGLGGSGGLGEGLSNALNDMLGGSLNTLGSKGGNNTTSTTNS 127	9
Db 1120	203 IGAPGVNGGAGGAGGTAGLFGNGGAGGAGGAGGAGGAGGAGGTGGSAGMLSGNGGDA 256	
Оу 328	8 LGASTMQISIGGAGGNNGLLGTSRQNAGLGGNSALGLGGGNONDTVNQLAGLLTGMMMMM 67	Qy
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Оу 225	06Bc	A;Genetics:
Db 980	tal source: strain H37RV	A, Exper
Оу 185		A; Residues:
Db 920	A:Status: preliminary; nucleic acid sequence not shown; translation not shown	A; Status
Qy 127		A; Refer
Db 865	537-544, 1998 Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell	Nature 393, A; Authors:
Оу 67	.; Davies, R.; Deviin, K.; Feltwell, T.; Senties, S., Rogers, J.; Rutter, S.; Seeger, K.; Skelton	Rajandream,
Db 822	C.; Harris, D.; Gordon,	R;Cole,
0у 7	17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000	C; Date:
Query M Best Lo Matches	RESULT 5 . \$70893 Strain H7RV) hypothetical glycine-rich protein Ryl058c - Mycobacterium tuberculosis (strain H37RV)	RESULT B70893 hypothet
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                                                                                                          230 NAGEGLDGSSLGGKGLGNLSGFFUPVGQLGHLVGTGGKKGGT-TLALHDIG 278
405 NGGNGGD----GGKG------GDAQLIGNGGNGGNGGKGGTGLMFGINCTG 445
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; preliminary; nucleic acid sequence not shown; translation not shown its type; DM OD. de: 1.191 (OA)02022; OB:AL12145; NID:91261554; PIDN:CAA17744.1; PID:9289 Amenial Source: Betain BFFP amily: collagen alpha 1(IV) chain

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P 9

25 ------GGOGGNAGTGL----DGSSLGGKGLQN-----LSGPVDYQQLGNAVGTGIGM 267 90 GGDGADAVNVVEMPTEPQ------AATGTAGSAGDPTGGNGGPGTPGSPMVAPPPP 1029 ?7 SPLDQALGINSTSQNDDSTSGTDSTSDSSDP--MQQLLKMFSEIMQSLFGDGQDGTQGSS 184 Match Conservative 24; Mismatches 180; Indels 116; Gaps 117; Conservative 24; Mismatches 180; Indels 116; Gaps MSMMGGGGLMGGGLGGGLGNGLGGSGGLGEGLSNALNDMLGGSLNTLGSKGGNNTTSTTN 126 GLGASTMQISIGGAGGNUGLLGTSRONAGLGGNSALGLGGGNONDTVNQLAGLLTGMMM 66 -----GNASATGTNGVANAGNGGKGGDGGQF-----GAGGNGGAGGSV--T 1119 -SGASGSGGNGGNAGTAGSGGAGGTGGTGLSGGNGGNGGNGGN----GGDGGNGAHGTVG 919 AGDAIN--NMALGKLGA 402 DKSWAKALSKPDDDGMTPASMEGENKAKGHIKRPMAGDTGNGNLQARGAGGSSLGIDAMM 387 KAGIQALNDIGTHRHSSTRSEVNKGDRAMAKEIGQFMDQYPEVFGKPQYQKGPGQEVKTD 327 TPITQVQQGGDGGAGGTGSTNANDGTATGGKGGEGGVGSILGGP-----GGNGGTG--- 1080 SGGK------QPTEGEQNAYKKGVTDALSGLMGNGLSQLLGNGGLG------ 224 AQFYPATSLFTFNGGAGGNGGTGSNGGAPGFAGAPGFTTGGNAGSQGIGGDGGNGGDGGK 979 -NATUGTI----AGQPAGGNGSAGGKGGDGGNIAAGA 1166 16,

TGTAGNGGNGGNGNDGA 1183

tical glyche-rich protein Bv357 - Mycobacterium tuberculosis (strain H37RV) es: Mycobacterium tuberculosis 17-Jul-1938 Heequence_revision 17-Jul-1938 #text_change 18-Reb-2000 S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon ion: F70971

A betree meriphering the Dology of Mycobasterium tuberculesis from the complete genome Alecessics; PFGGG, WANGE, MDC198525807 A Status; PFGLIBHANTY, nucleic acid sequence not shown; translation not shown Alecessics; PFGGGCACA, A Status; PFGLIBHANTY, nucleic acid sequence not shown; translation not shown Alecessics; PFGCACA, A SCROME references: GHALOZOZIZ; GBTWALIZ3456; HEDG1261554; PIDM:CAA17749-L; PED;223444 A SCROME TRESCHES STATAL BITRA ALIZ3456; HEDG1261554; PIDM:CAA17749-L; PED;223444 A Genes: NV5512 C:Superfamily; collegen alpha 1(1) chain; fibrillar collegen carboxyl-terminal homology;	HENGING 8 ### HENGING 1 #### HENGING 1 ##### HENGING 1 ###################################	QY 249 SERVINGOLGAN NETICIONALIZATORINESSIPAS PUNICIDENALE L'OLPHOUTE 308 1 1 0b 428 SIPEPANS - 081 OACIDAG	09 7-8 MOZ — «LAGIZIMICI/GESPAL ZORIZANI, ADMICI/ASSIGNATISTI/SERITAD [11] 0b 312 ADMICINATION (AND ADMICINATION CONTROLLARS (AND ADMICINATION CONTRO	C:Superfamily: unassigned collagens Genry Machine 11.94, Scooz 247, DB 2; Length 558; Best Local Similarity 20.48; Fred. No. 1.1e=08; Best Local Similarity 20.48; Fred. No. 1.1e=08; Best Local Similarity 20.48; Best Loc	Connor, R.; Davies, R.; Davies, R.; Davies, R.; Paltrell, T.; Gentles, S.; Banlin, R.; Bolrojd, S. Rajandess, M.A.; Bouses, J.; Butter, S.; Seeger, K.; Stelton, S.; Squares, S. Watter, P31, 319-44, 1398 [am., 1-1]. They are the control of the con
Outry Match 11.84, Score 246; DB 2; Length 1338; Watches 124; Conservative 137; Whenches 16; Todals 132; Cape 21; Oy 7; CLEASTHOLSTOAMSHELLDESUNGLEG	A Title: Deciphering the biology of workyler R.; Mintenson, S.; Marzell, B.G. Alfacterence number: A70500, MRID:95925987 octain Libercules is from the Complete geno Alfacterence number: A70500, MRID:95925987 octain Libercules is from the Complete geno Alfacterince; Marzellanty; nucleic acid sequence not shown; translation not shown Alfacterince; Telepismon, Alfacterince; Marzellant, Gardalizati, Gardalizati, RD:95261517, FIDN:CAM7117.1; FD:9536 Alfacterince; Marzellant, HFTRV C.Genetics; Alfacterince; Collegen alpha 1(17) chain	REBUR 9 PROMETED 4 PROMETED 5 PROMETED	07 232 TOYOGLGANGTGIOMOGIC (JAMESTERBILESTSSPINGERMARITIC) PROCESSES 311 Db 894	Oy 1.00 WTSTYRBELOALGLESSY	Query M Best Lo Matches 5 636 690

bb 182 σαργάσθαρα διανόμος με κατα με το μετα
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isla 1 yeller 71ch Frotein 15 yeller 71ch Frotein 17 yell 1998 seejmens. revi 18 yeller 1998 see hell 18 yeller 1998
Oy 371 LONGGOGGST-CTDNANADONINGKTCAN 403 Db 997 GGAGGAGNAYACTGL-ALMGCMGCMGCMGCMGSAN 631
OY 329 KSHAMALS
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Oy 154 SERMODILAMENSINGSIATROGISTOGROSSOGROPPEREROMAKENTRALGENAME 213 bb 412 AG
Oy 94 LABRILSKALARMALGESLATLGSKGONNTSTTISSPLOOALGINSTSONDOSTSGTDSTSD 153 Db 355 Ag-GLIJAANSALARTPSGANGGGGGANGBUT-GANGGANG-GHGGLVGNOOTGG 411 Db 355 Ag-GLIJAANSALARTPSGANGGGGGANGGGANGGANGGANGGANGGANGGANGGAN

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RESULT 11
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C;Genetics:
A;Gene: Rv0977
C;Superfamily: elastin
                                                       A;Cross-references: GB:AL021999; GB:AL123456; NID:g3261538; PIDN:CAA17576.1; PID:g291
A;Experimental source: strain H37Rv
                                                                                               A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA A:Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 NKAGMIKRPMGDTENGNICARGAGGSGLGIAMMGDAINNMLIGKE 401
352 NKAGMIKRPMGDTENGNICHARGAGGSGAGGAGA-RAG-ANGLANGNICH 414
414 --AGG-----HGGDPGLGG--AGGAGGASGGAGA-RAG--ANGLANGNDG 451
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RESIDE 12 P0956 Hypothetical glycine-rich protein RV2530c - Mycobacterium tuberculosis (strain H37RV) Cispecias Mycobacterium tuberculosis Cispecias Mycobacterium tuberculosis Cispeci 17-01-1988 Hespunce_revision 17-01-1998 Heart_change 24-Nov-1999 Ciscession: 77095 Ouery Main 11.8%; Score 245; DB 2; Length 923; Best Local Similarity 27.1%; Pred No. 4.2e-08; Best Local Similarity 27.1%; Pred No. 4.2e-08; Indels 110; Matches 146; Conservative 30; Mismatches 166; Indels 110; 442 -----GYPQQPAPQ--GLPIGTGGTGGE------GGAGGAGGDGGQGDIG---FD 480 293 DRAMAKEIGGEMDGYPEVEGKEGYGKGEGGEVKTDDKSWAKALSKEDDDGMTPASHEGEN 352 234 GLDGSSLGGKGLQNLSGPVDYQQLGNAVGT-GIGHKAGIQALHDIGTHRHSSTRSFVNKG 297 341 GDGQQGGAGGGGVGGGGAGGDGGAGGTGGTGGAGGNGSTGGAAGNGGNGGRGGAGGMATA 400 177 QDGTQGSSSGGKQPTEGEQNAYKKGVTDALSGLWGNG-LSQLLGNGGLG--GGQGGNAGT 233 289 GGAGGNGWAAEGITVGIGEOGGQCGDGGAGGAGGIGGSAGGIGG-----SQGAGGHG 117 GGNNTTSTTNSPLDQALGINSTSQNDDSTSGTDSTSDSSDPMQQLLKMFSEIMQSLFGDG 176 236 -----GANGMANGPAGGTGGIGGIGGIGGNGGVG-GHGSALFGHGGINGDGGTGGMGGQ 288 198 SGGIGGA-----GGAGGNGGLLFGNSGAGGQGGSGGLGGSGGT------ 235 353 KAKGMIKRP----MAGDTGNGNLQAR------GAGGS----SLGIDAMMAGDA 391 65 MMMSMMGGGGLMGGGLG--GGLG--NGLGGSGGLGRGLSNALNDMLG----GSLNTLGSK 116 5 TSGLGASTMQISIGGAGGNNGLLGTSRQNAGLGGNSALGLGGGNQNDTVNQLAGLLTGMN 64 GSDGGNGGGGG----NGGVGVGSAGGAGGTGGDGGAAGAG-----GAPGH------ 441 Gaps LY;

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Query Match 11.6%; Score 241.5; DB 2; Length 957; Best Local Similarity 25.8%; Pred. No. 7.3e-08;	Superfamily: elastin	Senetkes:	i 1-95 ferenc	Tritle: Inschiberting the biology of Myocharderium Abbrechais's Families complete genome Reference imber; A79500; MIDIOS293877 to the Abbrechaid from the Complete genome Accession; 170835 and A79500; MIDIOS293877 to the Abbrechaid from the Arborn Myochaid procession (MIDIOS) unclaid acid sequence not abovn; translation not abovn	*text_change 20-Jun-20 ., Churcher, C., Harris , Gentles, S.; Hamlin, K., Skelton, S., Square	ESULT 13 70825 State 13 State State	277 IG 278 601 VG 602	226	119 GTOSSESOGKOPTEGE-QNAYKKOPTEALSIJAGNOBSIJAGNOG	119 NATTSYTISELDOAGSINSTSQNDSTSGTDSTSDSSDPMQGLLXMFSELMQSLFGDQG-179 119 1	61 TORMONOSIMMOGICAGGIGNELASSIGGLESELSMALKIMLAGSITATLGSKOG 1.8 1	7 GLASTROLSICGAG-GENGLLGTSGONGLGGNSALGLGGGANTYNOLAGLL 60 1 1 1 1 1 1 1 1 1 1	Watches 91; Conservative 19; Mismatches 110; Indels 82; Gaps 14;		Gene: RP2634c Gene: RP2634c Superfamily: unassigned collagens	erences	ordered not stone, crambactor	anid segments not shown: translation not	Juliors: Sqares, R.; Solston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. Authors: Sqares, R.; Solston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. Reference number: AV950p, wuIIJ9829587	, R.; Parkhill, J.; Garnier, T.; Churche , R.; Devlin, K.; Feltwell, T.; Gentles, geers, J.; Rutter, S.; Seeger, K.; Skeltd	
9	B 5	Q 5	3 8	Query Best Match	A) Res A) Cr C) Ger C) Sug		Rajar Natus	C;Speci C;Date: C;Acces	RESULT H70663	B 8	₽ &	Db Oy	₽ 5	8	Q	Db	OV E	3 :	OV D	Oy Mat	
136 1		78 0	1 18	Query Mat Best Loca Matches	A:MOIECULE A;Residues: A;Cross-ref A;Cross-ref A;Experimen C;Genetics: A;Gene: Rv1: C;Superfami	Title: De Reference Accession Status: p	Rajandream, Rajandream, Nature 393,	C;Species: C;Species: C;Date: 17- C;Accession	10.11	691 0	665	631 :	578	818	164 1			408	362	Matches 2 :	

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GGIGGTGVLIGN-GGNGGSGGIGAGKAGVGGVSGLLLGLDGFNAPASTSPLHTLQQNVLN 517
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GGLFANGGAGGAGGFNA-AGGNGGNGGLFGTGG 722
                                                     GNLQARGAGGSSLGIDAMMAGDAINNMALGKLG 401
                                                                                                 EVECKPOYOKGPGGEVKTDDKSWAKALSKPDDDGWTPASMEQFNKAKGMIKRPMAGDTGN 368
                                                                                                                                                                                                            SLLIGSGGTGGNGGNSIGV-AGIGGAGGRG------GDAGL-----
                                                                                                                                                                                                                                                             QQLGNAVGTG-----IGMKAGIQALNDIGTHRHSSTRSFVNKGDRAMAKEIGQFMDQYP 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149;
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and sylvine rich protein pridde. Wrobesterium tuberculosis (erran HJ797)

"Williams and multiple rich protein pridde in the prid sferences: GB:283859; GB:AL123456; NID:g3261678; PIDN:CAB06114.1; PID:g17812 nntal source: strain H37Rv preliminary; nucleic acid sequence not shown; translation not shown n: H70663 1-515 <COL>

ily: Phaseolus glycine-rich cell wall protein

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13

ttch 11.5%; score 238.5; DB 2; Length 515; 21 Similarity 27.3%; Pred. NO. 5.5e-08; 109; Conservative 23; Mismatches 128; Indels 139; Gaps

GGAGGDAGLIGNG-GNGGIGGPGATGLAGG------AGGVGGLLFGDGGNGGAGGLG 197 GGAGGNNGLLGTSRONAGLGGNSALGLGGGNONDTVNOLAGLLTGNMMMMSMNGGGGLMG 77

TGPVGATG-GIGGPGGAAVGLFGHGGAGGAGGLGKAGFAGGAGGTGGTGGLLYGNGGNGG 256 GGLGGGLGNGLGGSGGLGEGLSNALNDMLGGSLNTLGSKGGNNTTSTTNSPL--DQALGI 135

Search completed: May 2, 2002, 03:35:44 Job time: 334 sec Db 789 ------GAGG-----AAPTGNG-----GAGGN------GGDALGLVGVGGNG 818

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346	286 770	231 726	177 679	118	61	7 21		196 NA: 196 NA: 299 253 Dyr. 253 Jyr. 254 Jyr. 255 Jyr. 257 Jyr	
ASMEDENKAKOMIKEPMAGDYGONGNLQARGAGGSSLGIDANNALGKLG 401	RSFYWKCDANAKELOGPKDYPEVFCKFQXQVGFGQBVKTDDXSNAKALSKFDDDGMTP 345	ACCIDENSIGNED AND THE PROPERTY OF THE PROPERTY	OCTYOGSSGGKOPTEGEDNAKKKGYPDALSGL-MANGLGOLGNGLIGGGGGGN 230 OCTYOGSSGGKOPTEGEDNAKKKGYPDALSGL-MANGLGLIGNGLIGGGGGNS 230 OCTYOGSSGGKOPTEGEDNAKKKGYPDALSGLNGCLIGGGGGNS 230 OCTYOGSSGGKOPTEGENNAKKGYPTANGLIGGGNGGNSGTN 725	GROGTGTASS PEGIALALGOANGOGAGTSGATGGAGGGGVPEGIAVLGLGEG-G-678	TREMONESMOGRAGIANGACIANKIAGSCALERILANANNMIAGSLATI-IASKA 117 TGALAANGGAAAGANTSGTG-GROGAAGGARGIIFALGANGAAGGDATGVGGRG 624	CICASTMOISTIGEAGGNN-CLLGTSRONALGCUSALGLIGGRONDTVNGLAGILL 60	Match 27.28; Peed NO. 127; Length 882; Ocal Similarity 27.28; Pred NO. 127; Length 882; St. 133; Conservative 37; Mismatches 128; Indels 139; Caps 23;	**************************************	- BI TONGGOO

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N116_YEAST
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| MSLATSGLGASTMOISIGGAGGNNGLLGTSRONAGLGGNSALGLGGNONDTVNOLAGLL 60
| MSLATSGLGASTMOISIGGAGGNNGLLGTSRONAGLGGNSALGLGGNONDTVNOLAGLL 60
     TGMMMMSMMGGGGLMGGGLGGGLGNGLGGSGGLGEGLSNALNDMLGGSLNTLGSKGGNN 120
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Score 2050; DB 1; Pred. No. 8.4e-113; 0; Mismatches 4;

Length 403; Indels 0;

Gaps

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310 GMIKSAIRGDTGNTHLSARGRGGASLGIDAAMIGDRIVNNGLKKLSS 350
                                                                                                                                  296 MAKEIGOFMDQYPEVFGKPQYQXGPGQEVKTDDKSWAKALSKPDDDGMTPASMEQFNKAK
                                                                                                                                                                                                           190 SPLQLONNGLQGLSGAGAFNQLGSTLGMSVGQKAGLQELNNISTHNDSPTRVFVDKEDRG
                                                                                                                                                                                                                                                                                                             144 GMSQQQGGLEGNKQPSSPEISAYTQGVNDALSAILGNGLSQTKGQ-----T
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                                                         356 GMIKRPMAGDIGNGNLQARGAGGSSLGIDAMMAGDAINNMALGKLGA 402
                                                                                                                                                                                                                                                               236 DGSSLGGKGLQNLSGPVDYQQLGNAVGTGTGMKNGTQALNDTGTHRHSSTRSFVNKGDRA
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HRPN_ERRCH STANDARD: PRT; 340 AA. 047278; 01-80V-1997 (Rel. 35, Created) 01-80V-1997 (Rel. 35, Last sequence update) 15-DEC-1998 (Rel. 37, Last amnotation update) ERWCH

Erwinia chrysanthemi. Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae: NCBI_TaxID=556; Pectobacterium

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STRAIN-EC16 / AC1450; SEQUENCE FROM N.A.

MEMLIARS-017240; bubbed-959405; liner A.; d the hypersensitive flauer D. N.; Wei I. M.; Beer S. V.; Oliner A.; d the hypersensitive flauer D. N.; which is the hypersensitive flauer to thouseed S.; except as the year Little Flauer C.; et al. (1998). Which is the hypersensitive flauer C.; et al. (1998). Which is the flauer C.; et al. (1998). Which is the flauer C.; et al. (1998). Which is the flauer C.; et al. (1998). The fl

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EMBL: L39897; AAC31978.1; -.

SEQUENCE Hypersensitive response. 340 AA; 34274 MW; E4D82C23731EF4C5 CRC64; GLY-RICH

owery Match 34.6%; Score 718.5; DB 1; Length 340; Best Local Similarity 42.6%; Pred. No. 19e-35; Matches 172; Conservative 41; Mismatches 114; Indels 77; Gaps

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Db 9 | 1 MOIST GGAGGNWGLLG/TSRQNAGLGG-NSA---LGLGGGNDDFVNGLAGLIGGNBOMM 67 | 1 MOITTKAHIGGDLGVSGLGJGAQGLKGLNSAASSLGSSVDKLSSTIDKLTSALTSMM--- 57

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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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KRBL_TaxiD=1773;
This swiss page entry is copyright. It is produced through a collaboration between the swiss institute of sixinformatics and the BMEL outstation the burspean skinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-i-SHILARTY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
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laboratory strains.":
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                     REGILES-935987, pubmed-9542430;
Goldo S.T., Brochs, Parkhill J. Garnier T., Churcher C., Barrist
Goldon S.V., Etglaster K., Gold S. (Berry Octh T.), Posado S.,
Barrist K., Goldon S., Goldon S.,
Barrist K., Falled T., Gestles S., Bellin N., Bolzod
Barrist Y., Japals K., Kroch K., McLenn J., Moule S., Murphy L.,
Gliver S., Galocine J., Guill M.A., Majandema M.A., Mogret J.,
Barrist Y., Sepper R., Malrion S., Majandema M.A., Mogret J.,
Barrist Y., Sepper R., Malrion S., Majandema M.A., Mogret J.,
Tockipheris J., Majandema M., Majandema M.,
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05 - Hov-1997 (ed.). 35, Last sepantro update)
10 - Hov-1997 (ed.). 35, Last sepantro update)
12 - Hould Call, (ed.). 140 - Last sepantro (ed.). 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 140 - 
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EMBL; AE006991; AAK45353.1;
                                                                              Propos; pp001223; PE; 1.
Hypothetical protein; Complete CONFLICT 218 218 T CONFLICT 235 235 G
                                                                                                                     PRINTS; PR01228; EGGSHELL
                                                                                                                                 Pfam; PF00934; PE;
                                                                                                                                         InterPro; IPR000084;
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          Local Similarity
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Conservative
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          31.8%;
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    70;
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  Gaps
    13;
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8 LGASTMOISIGGAGGNNGLLGTSRQNAGLGGNSALGLGGGNQNDTVNQLAGLLTGMMMMM
                                                NAGTGLDGSSLGGKGLQNLSGPVDYQQLGNAVGTGIGMKAG---IQALNDIG
                                                                                                 GGTGGGGGTGGNGGNGHAGGAGGSGGTAGLLGSGGSGGTGGDGGNGGLGAGSGAKG
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    NGGNGGD---
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                                                                                                                                                  SGGKQPTEGEQNAYKKGVTDALSGLMGNGLSQLL----GNGGLGGGQG--G
GGKG------GDAQLIGNGGNGGNGGKGGTGLMPGINGTG
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Matches 91
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InterPro; IRR001899; Gram_pos_anchor.
Pram; PR00934; PR; 1.
Probom; PR001223; PR; 1.
Probom; PR00123; PR; 1.
Probom; PR00123; PR; 1.
Probom; PR00123; PR; 1.
Probom; PR00123; PR00123;
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EMBL; AE007103; AAK47026.;
HSSP; P04002; late.
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laboratory strains.";
Submitted (APR-2001) to the
-1- SIMILARITY: BELONGS TO T
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Eleischmann R.D. Alland D., Elsen J.A., Carpenter L., Hhite O.,
Fleterson J., Debey R., Dodson R., Gwinn M.L., Raft D., Hickey
Rotorson J., Debey R., Dodson R., Gwinn M.L., Raft D., Hickey
Koloney J.F., Neison W.C., Gweldman J., Khouri R., Gill J., Mikula
Delbor R., Utterback T., Neidman J., Khouri R., Gill J., Mikula
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778 AA;
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Fleischimann R.D., Alland D., Eisen J.A., Carpenter L., Wh
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Delcher A., Utterback T., Weldman J., Khouri H., Gill J.,
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this sitis-page merry is copyright. It is produced through a collaboration between the suiss institute of sininformatics and the SML contention of its the buropean Michiformatics finititude. There are no restrictions on its use by non-profit institutions as long as its content is in only use by non-profit institutions as long as its content is in only many the content is no preserved, usage by and for commencial modified and this sattement is not removed, usage by the sub-channous conditions are present in some removal that in the content is not removed.
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                         MEDILME-959997, PubMed-9543430; Garnier T., Churcher C., Barristocke S.T., Broods, R., Barkhill J., Garnier T., Churcher C., Barristocke S., Berry C.Kh. T., Cabada F., Barristocke K., Barristocke S., Barris
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
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30-MAY-2000 (Rel. 39, Last sequence
20-MG-2001 (Rel. 40, Last amotatio
HYPOTHETICAL PE-PGRS FAMILY PROTEIN
RV3508 OR MTV023.15.
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HSSP; P19972; 1KVD.
TuberCulist; Rv3500; -.
InterPro; IPR000084; PE.
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Nature 393:537-544(1998).
-i- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match
Local Similarity 27. v
- 124; Conservative
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                                                                                                                                                                                                                                                                                                                                            GGAGGNAGFGAGVPGDG----GIGGTGGA 1519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DG------SSLGGKGLQNLSGPVDYQQ------LGNA 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SGGGGGFGGAMGKAGGGGMGGVGGDGGEGASGLGLGLSGFDGG0----GGQGGAGGSA 123:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMMGGGGLMGGGLG--GGLGN-GLGGSGGLG-EGLSNALNDMLGGSLNTLGSKGGNNTTS 123
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27.6%; Pred. No. le-1
tive 29; Mismatches
                                                                     Last sequence update)
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--- SIMILHATTY: BELONGS TO THE MYCOBACTERIAL PE FAMILY; PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-COC 1551 / Oskhosh:
Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Owinn M.L., Haff D., Hitchey,
Kolonsy J.F., Nelson W.C., Umyann L.A., Emplayers M.D., Salzberg S.L.,
Delcher B., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
nelson B.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corymebacterineae; Mycobacteriaceae; Mycobacterium
ACEL_TMXID-1732
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     LRMFSEIMQSLFGDGQDGTQGS--
                                                          GGDGGGGEFGAGGDGGAGGSGLTTGGA-AGNGGNAGTLSLGAAGGAGGTGGAGG
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31 914 WAG22 ANTIGEN
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Pred. No. 6.6e-07;
18; Mismatches 173;
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-- SSGGKQPTEGEQNAYKKGVTDALSGLMGNG
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
---SINILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY.
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WREI_RENTED-1774;

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STRAIN-CO 1501, Conhoell, Flater J.A., Carpenter D.

Petersbern, Deby A. Land drov R. Boulou R. Muchaeva M.D.

Rockons J.T., Nabou N.C., Emplay L.A., Emplayera M.D.

Rolcher A., Utterbeck F., Medden J., Khouri H., Call

Thous Sevene comperison of Myochesterium tuberculosis

Substituted (APP-2001), to the pseu/Amelana, yong-dackson

Substituted (APP-2001), to the pseu/Amelana, yong-dackson
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01.0CT-1996 (Rel. 34, Created)
01.0CT-1996 (Rel. 34), Last sequence update)
01.0CT-1996 (Rel. 34), Last sequence update)
02.040-2001 (Rel. 40, Last sequence update)
102.040-2001 (Rel. 40, Last sequence update)
103.000 (Rel. 40, Marcia) (Rel. 40, Last sequence update)
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Pfam; PP00934; PE; 1.
ProDom; PD001223; PE; 1.
Hypothetical protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TubercuList; Rv1325c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z73902; CAA98089.1;
EMBL; AE007010; AAK45630.:
HSSP; P19972; 1KVD.
TIGR; HT1367; -
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TO THE MYCOBACTERIAL PE FAMILY. PGRS
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                       Score 229.5; I
Pred. No. 9.6e
32; Mismatches
                                   32;
                                                                                                                                                                      POTENTIAL PE-PORS
HYPOTHETICAL PE-PORS
RV1125C.
GLY-RICH.
G -> V (IN REF. 2).
G -> D (IN REF. 2).
G -> D (IN REF. 2).
L -> F (IN REF. 2).
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No. 9.6e-07;
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aft D., Hickey E.,
wa M.D., Salzberg S
, Gill J., Mikula A
                                                                                        Length
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laboratory strains.";
Submitted (APR-2001) to the
-:- SIMILARITY: BELONGS TO
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                                                                      Peterson J., DeBoy R., Dodson
Kolonay J.F., Nelson W.C., Umu
Delcher A., Utterback T., Weld
Bishal W.;
                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D.,
                                      "Whole genome comparison
laboratory strains.";
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                                                      of Mycobacterium
                                                                                         D., Eisen J.A., Carpenter L., White O.,
odson R., Gwinn M.L., Haft D., Hickey E.,
Umayam L.A., Ermolaeva M.D., Salzberg
Weidman J., Khouri H., Gill J., Mikula
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THE MYCOBACTERIAL PE FAMILY.
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                                                                             n M.L.,
Ermolaeva
                                                          tuberculosis clinical
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RESULT 15
GRP1_EFTEY
ID GRP1_E
AC P09789
DT 01-MAA
DT 01-AU
DT 01-AU
CRP-1.1
GN GRP-1.1
GN GRP-1.0
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Best Local Similarity 29.4
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HSSP; P19972; 1k
TIGR; MT2159; -.
                                                                                                                                                    UI-MAR-1989 (Rel. 10, Created)
OI-MAR-1989 (Rel. 10, Last sequence update)
OI-MOR-1982 (Rel. 22, Last annotation update)
GLYCING-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR
GRI-CING-RICH CELL WALL STRUCTURAL PROTEIN 1
                                                                                                                                                                                                                    GRP1_PETHY
P09789;
01-MAR-1989
01-MAR-1989
01-AUG-1992
Deciunia hybrida (Petunia).
Bakaryota: Yiridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: sudicotyjadons: core endicots:
Asteridae: eussterids i: Solanales: Solanacese: Petunia.
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Hypothetical 312 313 20mplete proteome.

CONFLICT 312 312, 41979 MW; 12C8630C59CAOC13 CRC64;

SEQUENCE 491 AA; 41979 MW; 12C8630C59CAOC13 CRC64;
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InterPro; IPR000084; PE.
Pfam; PF00934; PE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                469
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CAUTION: REF. 1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 59, REF. 1 SEQUENCE HAS BEEN CHECKED BY AUTHORS IN REF. 1 AND THEY REPORT THAT NO ERRORS HAVE BEEN COUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPG 471
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29.2%; Pred. No. 8.3e-07;
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7; Mismatches 111
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"Genetic Organization of the hpr gene Cluster and deptr

Exvisia horbicola pv. gypeophilme."

Schmitted (MN-2001) to the Besil/Geneshn/pD8J databases.

BESEJ, AR271715; AR25432.11: 6279885DD95Ac2A CRC64:
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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319 SAMAGDNGNIKIQARGAGGSSKGIDATLYGDALRHALTRISAA 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                     79 Match 28; Score 1002.5; DB 2; Length 365; Local Similarity 57.98; Pred. No. 5.98-63; Score 223; Conservative 40; Mismatches 83; Indels 39;
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                                  KAKGMIKRPMAGDTGNGNLQARGAG 377
                                                              URSLAKEVGGFMUGYPELFGRPGYGKTPYSDVKTDTKSWAEALSNPDDDGHTPASMEGFN
                                                                                                                                                                                                                                                G----AGSSLDKALDL------DPTADGGGLSDSNGTYGMSPIDQLMKMFAEVMQSM
                                                                                                                                                                                                                                                                                                               TAMMMMNNWAGGSGL-GGGLGTA-GGELGGQSGGALGGPLYGNQGGQLGGALGTSLGGTG
                                                                                                                                                                                                                                                                                                                                           TGMMMMMMGGGGLMGGGLGGGLGNGLGG--SGGLGEGLSNALNDMLGGSLNT-LGSKG 117
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                                                                                                                                                                                        FG-GQGDTSGRGT-GNQPTPDEQNAYTKGVTDALTAVMGGGLSQMQGS-GTGGGMNGSIG
                                                                                                                                                                                                                                                                                                                                                                          MSLNTTPLGIPAMQISL---GDSNGLPGPNLQNAVLN----SNGDRSTDETINQLAGAL 52
                                                                                                                                                                                                                                                                                                                                                                                                         MSLNTSGLGASTMQISIGGAGGNNGLLGTSRQNAGLGGNSALGLGGGNQNDTVNQLAGLL
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Best Local Similarity
                                                                                                                                                                                                                                                                                       Q9LAW6;
Q9LAW6;
01-OCT-2000
     SEQUENCE FROM N.A
STRAIN-EA246;
                                                                                                                              Erwinia amylovora.
Bactería; Proteobactería;
                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
HARPIN HRPH (FRAGMENT).
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SEQUENCE 344 AA; 34493 MN; 137E535659D1CEFO CRC64;
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"HrpN of Erwinia chrysanthemi 3937
regulation.";
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01-MAR-2001 (TrEMBLrel.
HARPIN PROTEIN.
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                                                                         NCBI_TaxID=552;
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NCBI_TaxID=556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEIGQFWDQYPEVFGKPQYQKGPGQEVKTDDXSWAKALSKPDDDGMTPASMEQFNKAKGM
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                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Pred. No. 2.7e-44;
                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                              subdivision;
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                                                                                                                              Enteropacteriaceae
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B 5	OY 3 LATSGLGASTAMO1	
Mat Bes	12.7%; Score 264.5; DB 2; Length 1489; 26.1%; Pred. No. 2.2e-10; attive 27; Mismatches 149; Indels 153; G	
4 58 5 5 7 7 7 7 7 7 8 9 8 7 7 7 7 7 7 7 7 7 7 7	DOSINGS DOSINGS DOSINGS DOSINGS PRELIMINATY: PRT. 1489 A. DOSINGS DOS	
Q B	DY 382 GEDAMAGGALINMALGECICA 403 . DB 121 GEDAMAGGALINMALGECICA 142	0 0
Q B	OY 322 OPYKTODKSHAKLSKEDDOCHTPASHEQPHKAKOHTKERMÁDTONOHLÁJARGÁGGSEL 181 DD 61 QEYKTDDKSHAKALSKEDDOCHTPASHEQPHKAKOHTKSHMÁGDTCHCHLJARGÁGGSEL 120	₽ 5
Q B .	262 1	무양
Q B 4	Owery March 91.24, Score 712, DB 2; Length 142; Best Local Similarity 97.24, Pred: No.ch 92-45; Length 142; Marches 138; Conservative 97, Mismacches 4, Indels 0; Caps 0;	
	A Kim J.F., Laby R.J., Boor S.Y., restant of two Ervinia amployora comparison of the Ervinia comparison of the E	SORRERA
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1160 GIAGDGGPGGDG--GNAGVGGKGGTNGNGGSGGTGGTGGAGGNAGAGGLANTGGTA---- 1213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1268 GGAGGGGGAGGAGISFSNGSNGGTG 1292
                                                                                            1244 AGGPGG-------KGGAGGNAGTGGTNGSGA 126
                                                                                                                                     317 OKGEGGEVKTDDKSWAKALSKEDDDGHTPASMEQFNKAKGMIKREMAGDTGNGNLQARGA 376
                                                                                                                                                                                                                                  257 LGNAVGTGIGMKAGIQALNDIGTHRHSSTRSFVNKGDRAMAKEIGQFMDQYPEVFGKPQY 316
                                                                                                                                                                                                                                                                                                                         205 ALSGEMGNGLSOLLGNGGLG------GGQGGNAGTGLDGSSLGGKGLQNLSGPVDYQQ 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 LGGSGGLGEGLSNALNDMLGGS--LNTLGSKGGNWTTSTTNSPLDQALGINSTSQNDDST 145
                                                  377 GGSSLGIDAMMAGDAINNMALGKLG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 AGLGGNSALGLGGGNQNDTVNQL-----AGLLTGMARRAMSHMGGGGLMGGGLGGGLGNG
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007224, 007024 (007024) 01-UL-1997 (TERMELTEL. 04, Created) 01-UL-1997 (TERMELTEL. 04, Last seguence update) 01-UL-1997 (TERMELTEL.) 17, Last annotation update) HYPOTHETICAL 49 l MOA PROTEIN. 007224 PRELIMINARY; 591 AA

NCBI_TaxID=1773; Mycobacterium tuberculosis. Bacteria; Piracutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. RV0297 OR MTCY63.02.

STRAIN-H37RV SEQUENCE FROM N.A.

Williams Signature (1982)

State Signature (1982)

Tuberculist; Rv0297; -.
InterPro; IPR000084; PE.

pfdam; PF00934; PE; l. Complete proteome. Hypothetical protein; Complete proteome. SEQUENCE 591 AA; 49058 MW; 4E4675EDD4297F5A CRC64;

Jery Match 12.38 ast Local Similarity 26.88 atches 123; Conservative 12.3%; Score 255; DB 2; Length 591; 26.8%; pred. No. 3.4e-10; vative 24; Mismatches 168; Indels 1 Indels 144; Gaps

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Query Match
Best Local Similarity
Matches 96; Conserv
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CODE ST. RECORD, Parkhill I. Gernier T. Churcher C. Harris D.
CODE ST. RECORD R. Parkhill I. Gernier T. Churcher C.
Badcock K. Masham D. Brown D. Chilingworth T. Comnor R.
Badcock K. Masham D. Brown D. Chilingworth T. Comnor R.
Corners T. Chapter S. Record D. Chilingworth T. Comnor R.
Corners T. Chapter S. Record D. A. McCham J. Mayla B. C. Merphy J.
Marter S. Seeper K. Selton S. Signares S. Selton S. Series R. Salton J. E.
Taylor K. Milcheld S. Burrel B G. T.
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                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00934; PE;
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Interpro; IPR000173; PfkB.
                                                                                                                                                                                                                                                                                Prodom; PD001223; PE; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TubercuList, Rv3388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTGNGNLQARGAGGSSLGIDAMMAGDAINNMALGKLGAA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GVG------GAGAAGAIGGHGGDG-------GSVNTPIGGSEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVEGKPQYQKGPGQEVKTDDKSWAKALSKPDDDGMTPASMEQFNKAKGMIKRPM----AG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDSGNGGAGGDG---GAGVSATDIAGTGGRGGNGGHGGLWIGNGGDGGAGGVG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TG - - GNGGVGAPGGAGGNGGHVSGGSVNTAGAGGKGGNGGTGGAGGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAANGGNGLNLYGYPGTAGGGADGANGSAIGQAGGAGGDGGNASTSGGIGIAQTGGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P03622;
                                                                                                                                                                                                   E 731 AA;
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                                                                                                                                                                                                   60454 MW;
                                  28.7%;
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Pred. No. 1.2e-09;
23; Mismatches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
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Conservative

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Gaps

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Mismatches

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Gaps 864 66

Matches

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x windings/spi599]; nuhwdes/s4200;
xx color 57. Rosed R., Furbhill J., darnier T., Churchet C., Harris D.,
xx color 57. Rosed R., Furbhill J., darnier T., Ellings R.,
xx color 57. Rosed R., Furbhill J.,
xx color 57. Rosed R.,
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                                               Best Local
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01-UN-1998 (Tribulcal. 06. Created)
01-UN-2001 (Tribulcal. 07. Lais emphase update)
01-UN-2001 (Tribulcal. 17. Lais emphase update)
01-UN-2001 (Tribulcal. 17. Lais emphase update)
01-UN-2001 (Tribulcal. 17. Lais emphase update)
02-UN-2001 (Tribulcal. 17. Lais emphase update)
02-UN-2001 (Tribulcal. 17. Lais emphase update)
03-UN-2001 (Tribulcal. 17. Lais emphase updated)
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hes 117;
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                                               26.8%;
                                               Score 248; DB 2;
pred. No. 2.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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192 BCBQNAYKKGYTDALGG-LMGNGSLGCLGGKGLQNL 148
425 GCRGGDGGSGCAGGASGMLMGNG-GNG-GNGTGGSGCVGGNGGIGGDGAG-GGNATSTS 481
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                                                                   369 GNLOARGAGGSSLGIDAMMAGDAIN 393
                                                                                                                                523 -----AGCHANSGNGGGGGTGGAGGTHG-TPGSGN-------AGGTGT 55
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                                                                                                                                                                                                   EVFGKPQYQKGPGQEVKTDDKSWAKALSKPDDDGWTPASMEQFNKAKGMIKRPMAGDTGN 368
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PROSITE; PS00318; HMG_COA_REDUCTASE_2; UNKNOWN_1 Complete proteome. 1079 AA; 81163 MW; A79718CDCB74B97D CRC64;

Query Match 11.99 Best Local Similarity 26.29 Matches 118; Conservative 11.9%; Score 246.5; DB 2; Length 1079; 26.2%; Pred. NO. 2.8e-09; Live 26; Mismatches 164; Indels 143; Indels 143; Gaps

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	180 TOGSSSGGKOPTEGEQNAYKKGVTDALSG	Qy
	244 GYGGYGAAGANGATPGQDGAAGYAGSDDGAGGDGLAG 280	망
	QNDDSTSGTDSTSDSSDPMQQLLKMFSEIMQSLFG	õ
	189 GGGVGGMGGAGGGAGGAAGAAGLEGNGGAGGAGGAGGAGGAGGNAGWFGHGGAG 243	₽
	67 MSHMGGGGLMGGGLGGGGLGNGLGGSGGLGEGLSNALHDMLGGSLNTLGSKGGN 119	Q
	7 GLGASTMOISIGGAGGNUGLLGTSRONAGLGGNSALGLGGRONDTVNOLAGLLTGM999 66 1 1 1 1 1 1 1 1 1 1	용 왕
20;	Local Similarity 28.0%; Préd. No. 5.5e es 115; Conservative 21; Mismatches	zœ
	y Match 11.8%; Score 245.5;	0
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	PROSITE: PS00583; PEKB_KINASES_1; UNKNOWN_1. PROSITE: PS01287; RTC; UNKNOWN_1.	무무

OSSRES PRELIMINARY, PRT, 882 AA.

O'-UMP-1998 (TribMirel: 06, Created)
O'-UMP-1998 (TribMirel: 06, Late sequence update)
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SEQUENCE 882 AA; 71699 MW;

336C6A9D005F3706 CRC64;

GGDS 540	481 GGRGGDGGPGGGGAGGDGSGTFNAQANNGGDGGAGGVGGAGGTGGTGGVGADGGRGGDS 540	481	рb		
AGDA 391	KAKGMIKRPMAGDTGNGNLQARGAGGSSLGIDAMMAGDA 391	353	9		
FD 480	GYFQQPAPQGLPIGTGGTGGEGAGGAGGDGGQGDIGFD 480	442	망	_	
EQFN 352	DRAMAKEIGGENDQYPEVFGKPQYQKGFGQEVKTDDKSWAKALSKPDDDGWTPASHEQEN 352	293	Qy		
441	GDGGNGGGGGNGGVGVGSAGGAGGTGGDGGAAGAGGAPGH	401	Db		
VNKG 292	234 GLDGSSLGGKGLQNLSGPVDYQQLGNAVGT-GIGMKAGIQALNDIGTHRHSSTRSFVNKG 292	234	Qy		
MATA 400	GDGGQGGAGGSGGVGGGGAGAGGDGGAGGTGGTGGAGSTGGAAGNGGNGGRGGAGG	341	Db		
NAGT 233	177 QDGTQGSSSGGKQPTEGEQNAYKKGVTDALSGLMGNG-LSQLLGNGGLGGGQGGNAGT 233	177	9		
GGHG 340	289 GGAGGNGWAAEGITVGIGEQGGQGGDGGAGGAGGIGGSAGGIGGSQGAGGHG 340	289	Db		
FGDG 176	117 GGNNTTSTINSPLDQALGINSTSQNDDSTSGTDSTSDSSDPMQQLLKMFSEIMOSLFGDG 176	117	Qy	_	
MGGQ 288	GGAGMAAGPAGGTGGIGGIGGIGGAGGVG-GHGSALFGHGGINGDGGTGG	236	Db		
LGSK 116	65 MOMSMAGGGGLAGGGGLGGGLGNGLGGGGGGLGBGLSNALNDMLGGSLNTLGSK 116	65	Qy		
235	SGGIGGAGGAGGNGGILFGNGGAGGQCGSGGIGGSGGT	198	Вb		
FGMM 64	5 TSGLGASTMQISIGGAGGNNGLLGTSRQNAGLGGNSALGLGGGGNQNDTVNOLAGLLTGMM 64	u	Qy		
Gaps	Quary Match 11.9%, Score 245, DB 2, Length 923; Best Local Similarity 27:1% President 29:09; Indels 110; Gaps Matches 114; Conservative 30; Mysmatches 116; Indels 110; Gaps	ry Ma t Loc ches	Que Bes Mat		
	PROSITE: PROUTA:: AST_ROIENDE. GENERALE. GENERALE. COMPLETE PROTECTION. 81604 MW; 036E2085E48C033 CRC54; SEQUENCE 923 AA; 81604 MW; 036E2085E48C033 CRC54;	Complete SEQUENCE	SON	-	

Ouery Match 11.5%; Score 238.5; DB 2: Best Local Similarity 27.2%; Pred; No. 7.9e-09; Matches 113; Conservative 36; Mismatches 128;

Length 882; Indels 139; Gaps

23;

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SEQUENCE 714 AA: 59990 MW; E66D2A7FA25CF0E1 CRC64;	PS005	R000084; R002173;	mature 393:537-544(1998). EMBL: AL022022: CAA17748.1: Tuberculist: RW3511:	of Mycol	Squares S., Sqare B.G.;	Jagels K., Krogh A., McLean J., Moule S., Murphy L., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,	Chillingworth T., Connor R.,	987; PubMed-9634230; osch R., Parkhill J., Garnier T.	SEQUENCE FROM N.A. STRAIN-H37RV:	ACCINOMYCETALES; COTYNEDACTETINENE; MYCODACTETIACENE; MYCODACTETIUM. NCBI_TaxID-1773;	utes; Actinobacteria; Actinobacteridae	FORD-FAMILE PAUTOLIA. RVSSI1 OR MITVO23.18. MUTONBOTERIUM TUDDETCHIOGE	(TrEMBLiel. 06, Created)	083856 PRELIMINARY; PRT; 714 AA.	56 15	789GAGG	GGSSLGIDAMMAGDAINNA	286 RSFWKGDRAMAKEQPMDQKPEYFGKEQYQKGQBYKTDDKSMAKALSKDDDGKTP 345 770DGDGGGEAVAVGIAVG	72b TGTGGNGGAGGGGLSSPVILGIGIGGAGGDGGGALGVLGGMGG 769	AGTGLDGSSLGGKGLQNLSGPVDYQQLGNAVGTGTGNKAGTQALNDIGTHRHSST	ANGAGGAATGDGATGGAGGFGGAGAGIANFLGFSVLHGGAGGAGGTA	177 ODGTOGSSSGGKOPTEGEONÄYKKGYTDALSGLMGNGLSQLLGNGGLGGGQGGG 230	118 GRNETSTTNSPLDOALGINST-SONDDSTSGTDSTSDSSDPMOOLLKMFSEIMGSLFODG 176 625 GROOTGTASSPEGTARAGGAGGQGGAGTSGTTGAGGGGCDCVFEGIAVLGLGFG-G 678	61 TOMMONISMICGEGLANGGILGGGILGANLIGGGGGGISBALN-DHLGGSLAT-LISKG 117	7 GLASTMOISIGAGONN-CLLGTSRONAGLGONSALGIGONONTYPOLAGIL 60 51 GGGASVOTOGSGGAGGIOFGFVGAGGNOGNAGTGVGVNNANGGN	

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                                                                                                                                                                                                                                                                411 GAGGQAALLEGRGGTGGAGGYGGDGGGGGGGGGTGGT-----GGAP 465
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                                        381 L-GIDAMMA 388
                                                                                525 -----GDGG-----NGGGSGASQGNGGNGGNGGTGGKGGTGGAG 558
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Search completed: May 2, 2002, 03:36:49 Job time: 274 sec



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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE BASE COUNT ORIGIN	RESULT 1 AND 598 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM		44	c 42	41	. w	c 37	36 36	34.5		c 30	29		n 26									i jua :	10 9			12		2 -	Result No. S
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61 GAGGAATACGTTATGAGTCTGAATACAAGTGGGCTGGGAGCGTCAACGATGCAAATTTCT 120
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1 (base) 1 to 128
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Sequence 4 from patent US 6235974.
AR153832
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Оy	Фb	Оy	Db	Qу	Db Qy	Оy	Db Qy	Db Oy	Db Oy	DЬ	Оy	Dβ	Db Oy	Qу	Оy	D Oy	Db
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RESULT 5

Ouery Match Best Local Matches 128 Oy 1 mag Db 1 Amag Oy 61 gag Oy 61 Gag Ob 61 GAG	gene CDS BASE COUNT	JOURNAL REPERBOCE AUTHORS TITLE JOURNAL REPERBOCE AUTHORS TITLE JOURNAL REMARK REPERBOCE AUTHORS JOURNAL REMARK REPERBOCE AUTHORS JOURNAL REMARK REPERBOCE AUTHORS JOURNAL REMARK REPERBOCE AUTHORS JOURNAL REMARK REPERBOCE AUTHORS JOURNAL REMARK REPERBOCE AUTHORS JOURNAL REMARK REPERBOCE AUTHORS JOURNAL REMARK REPERBOCE AUTHORS JOURNAL REMARK REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE JOURNAL REPERBOCE JOURNAL REPERBOCE AUTHORS JOURNAL REPERBOCE JOURNAL REPERBOCE JOURNAL REPERBOCE JOURNAL REPERBOCE JOURNAL J	ERWHARPIN LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS
Vanich malarity 99.5% Score 1281.6; DB 1; Length 128; Cool Smilarity 99.5% Score 1281.6; DB 1; Length 128; Cool Smilarity 70.7; Predictors 92.5; Indels 0; dages 0; lassiches 4; Indels 0; dages 0; lassiches 10; Length 128; Cool Smilarity 129; Cool		USA. Cornell University USA Cornell University Cornell University ared by submitten Cornell University DEA Phaced gi:3417261.	ESMIANTI 1288 by IDAN 10790 amployone http://dispression.complete.cds. 107290, amployone 107290, 20714399077 NATURE OF THE OFFICE OFFI

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Best Local Similarity 99.9%;
Matches 1158; Conservative
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Hypersensitive response induced resistance
Patent: US 5776889-A 4 07-JUL-1998;
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BASE COUNT ORIGIN

REFERENCE AUTHORS TITLE JOURNAL KEYWORDS SOURCE ORGANISM ACCESSION VERSION RESULT AR016697 LOCUS D 8 문 8

DEFINITION

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FEATURES Source

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/COUCH_Staff=1 /transl_table=11	
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RIONSEWDCIMYSLNNALKSFKHHDEYTARLHKGEKIPVDAEFFKHAQSKSMVEGLPH	

// Authorities the state of the	JOURNAL Shafted (25-300-2000) Plant Pathology, The Ohio State University, 2021 Coffey Rd. Columbus, OH 422[0-1887 USA COMMENT On Aug 32, 2000 this sequence version replaced gi:148500. FRATURES A LOCATION/QUALIFIERS SOURCE 1. 20000	SEE	JOHRADIA MAJ. MICHORIOLO (3), 477-485 (1993) MEDIANE 940156-0 (1993) MEDIANE 950156-0 (1993) MEDIANE 9	REPERRORE 1. (Dasses 357) to 5863) ANTHONES Frequentick, R.D., Majerczak, D.R., and Copilin, D.L., Eryinia stewartii Mrža, a positive regulator of pathogenicity of Hittle Extension, 18 staniari to Secondomonas Syringes pr. phaseolicola Hittle Gestion, 18 staniari to Secondomonas Syringes pr. phaseolicola	ACTESSION AP\$28357 (AGA9) VERSION AP\$28357.1 G13885229 VERSION AP\$28357.1	RESULT 11 AF224257 LOGUS AF224257 DRFPHYTON Pentoses stewartil subsp. stewartil hrp gene cluster, partial	Oy 1276 geggettaaget 1287 	0/ 1156 angangnya makangpananganantangangangpangpangpangpangpangpangpangpan	Oy 1096 genetgenecegoegtettgegegttenecenggesegggestgetenessgece Db 241 GEANTGHEAUCAGCAGTATGERGCAGTTCAACAAGCCAGGGCATGATCAAAGCGCC	DE	
P STOWNIES OF STOWN CDS	ne Ohio State University, SA seed gi:148500.	til adasp. stewartil hrp hrpA, hrpC, hrp8 and wtsE hrroyo-Rodriques.A.S.,	RBS gene GDS	D.L. pathogenicity gene	n: Enterobacter(aceae;	CDS 23-MG-2000 CDS ecluster, partial	RBS		Catgatcaaaaggccc 1155 CDs CATGATCAAAAGCCCC 300	CCACADANGCCCGGGT 180 promoter casgccagatgacgac 1095	
(37) - (34) (38) - (34) (39) - (39) (39)	GTTKNIMPETLALHEN, MENGAL KERLI SKIT FALF ILLI MENGANGKA GIJAK KANANA GTTKNIMPETLALAH KEN KENGET LOMA KADI, YEN MESKANGKI JAJOLATAK KADI, M IKLANGISY MSI JADILAI SINTYSTHINALI MEKMETTINATYKYA I SHHIJI S 4337 3512 / Jadie - "https" / note-"trps"	/hois-"picitive response regulator" /rodo_start- /rodo_st	2856, 2861 /genee* http:// 2856, 2500 /genee* http:// /genee* http://	VECOSY PARTENDADE EMMANA PRODUCT OF THE WARK LESSHARI ALL VECOS STATES OF THE WARK LESSHARI ALL VECOS STATES OF THE WARK LESSHARI ALL VECOS STATES OF THE WARK LESS OF THE WARK	// CADIACT-"HEPS" // CADIACT-"	/hote-"ris" 180837 /gene-"hry" /note-"putative sensor kinase" /hoten_sart-11	1370 No.1376 No.1444	/transi_ball_all_all_all_all_all_all_all_all_al	690-1116 /gene-intpr /gene-intpr /note-alternate sigma factor*	Complement(443. 472) /note="High-dependent" 677. 1236 /dene="hiph." 677. 682	LLEHPOHAOLETONOKNOTLLORSPAPDLDALLDVAGKDP*

9	/translation="MPFSDNARLRWLRWWCIDSWLTADKSWRYAAFYDLDEARLSALA	
DŁ		
9	/transl_table=11	
Db	/yeller http: /note="type III secretion protein"	
9	/986.7567	CDS
Dt.	79000 11000 6974 - 17567	gene
g g	/note="Region: transmembrane domain" 6974. 6980	RBS
Db	6859. 6921 /gene="hrcJ"	misc_feature
ō,	PDVIEPRIROMVASSLPGLAGRPGKDLAIVEVPAGTIQUKESEVSEGPETVIFQRAIQ LTWLSGTIGTLILLAVAASVGLPYWRRYHQRKKTESDEKGE*	
Db	YHIKAEKHTUKDGITVAVDTADLURAVHILDAAGLPRETRTULGEVFOKUGVISTPLE ERARYIYALSQEVESTLSQIDGVIVARVHVVLPERVAPGEPILPASAAVFIKYKPELD	
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₽	6205 6264	sig_peptide
9	62056984 /gene="hrcJ"	gene
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	55385600	misc_feature
- 11	5525 5531	RBS
	55255771	gene
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	VATOKPLITLYEGGTFRRDLYFRLNTLSIQLQPLRSQVEIIIFLFRHFIAKAATTMQC TPPEITORLGEYLSYSMPGNIRELKTAAKRFTLGLPPLNVPRNAERQGPQLKEILRR	
_	AVOARAGYTERANNETT.FT.DETDSMPLST.OAKLLRVLENRGIERLGGTRFIPVNMRVI	

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opery MACCh 30.7%; Score 395; DB 1; Length 20000; Best Local Similarity 63.1%; Pred. No. 3-9e-85; Matches 775; Conservative 0; Mismatches 385; Indels 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11796 CTTT-----GGGTGGCAATANTGGTTTGATGGGAACGGATTTACGTACCGACGGAT 11846
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536 gcgacccgatgcsgoagctsgttggts 935
12165 g---TCGGATGAAACAGTTGATGAAAATATTCGCCGATATTACGCAAAGCCTGTTTGGCG 12221
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                                                                                                                                                      12450 AGCAGTTGGGTAATGCGATCGGTACCGGTGTCGGTATGAAAGCCGGGCATTGAGGCCCTGA 12509
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956 cgatggcgaaggaaatcggtcagttcatggaccagtatcctgaggtgttttggcaagccgc 1015
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	Query Ma	COUNT	gene	MEDILINE PUBMED REFERENCE AUTHORS TITLE JOURNAL FEATURES	VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	Db 12870 RESULT 12 AF271716 LOCUS DEFINITION ACCESSION	1196 12810 1256	1076 12690 1136 12750	12570 1016 12630
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		326		55 A	AF271716.1 Erwinia he Erwinia he Erwinia he Bacteria; Pantoea. 1 (bases Mor.H., Ma Genetic or Erwinia he Mol. Plant	GGCACTGACO GGCACTGACO AF271716 EIWinia AF271716	gtgccggtggttcttcgctgggtattgatt 	aagcc 11 11 CAACC atgat 11 11	GGCCAG
		/code /tram /pro /pro /pro /tram /tra /tram /tra /tram /tram /tra /tra /tra /tra /tra /tra /tram	/orga /orga /note 103.		herbic herbic herbic prot prot s 1 to Manuli organi herbic nt Mic	CAGACTGAG	ATCATO	agatga AGACGA 	aggccc
	27.48	rtrans Lables (rodon_start=1) (rotot_i = harpi (rotot_i = dranpi (11249 //organ.sm="Erwinia /db_xref="taxon:48 /note="pathovar: g /note="brpw" /gene="hrpw" /gene="hrpw"	uses to 1249) when to 1249) when wor, H., Barash, I. a tt Submission tt Submission tttod (24-MAY-2000) Plan 69978, Israel Location/Chalifiers	.6.1 GI:8547352 herbicola pv. 9yps herbicola pv. 9yps a; Proteobacteria; ies 1 to 1249) Henulis, S., Zuck, M organization of th organization from herbicola pv. 9yps ant Microbe Interna	TGAGTGC	ogetgg NATGC	argacg Argacca Jgccca	ngggac ngggtc
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Query Match Best Local Si Matches 336;	BASE COUNT	gene CDS	JOURNAL REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	x x w	Db 1127 AAGGO Oy 1220 ttga:	1007 1100 1067
18.7%; Score 241.2; DB 1; Løngth 1035; DS. Mainterty 68.0%; Proceed 241.2; DB 1; Løngth 1035; 336; Conservative 0; Mismatches 198; Indels 0; Gaps 0;	// MIDCLIDE* PURALIVE FOLE IN PATROMORIOLEY IN CHICORY // MIDCLIDE* PURALIVE FOLE IN PATROMORIOLEY IN CHICORY // TURNIL_MAN HE - TO COME IN // PROCEDIA_L IN CONCENTRY // PROCEDIA_L IN CONCENTRY // PROCEDIA_L IN CONCENTRY // TURNIL MAN HE - TO CONCENTRY AND HE - TO CON	terium chrysanthemi" "	UnDebassMe to 1035) Boccate M. Bo	Erisid2027. 1035 bp DNA . Bristal chrysantheal hrp# gene for harpin protein. 10027. cg:1305412 harpin protein thrw gene. harpin protein thrw gene. Marpin protein thrw gene. Becchokectim chrysantheal. Becchokectim chrysantheal. Becchokectim. 10027. data protein gene aubdivision; Enterobacteriaceae; Becchokectim. 10028. data protein chrysantheal. 10028. data protein chrysantheal. 10028. data protein chrysantheal. 10038. data protein chrysantheal.	CHILD BEILD	

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784 tcgtcgctgggcggcaaagggctgcaaaacctgagcgggccggtggactaccagcagtta 843

gene CDS	RESULT 14 ENTHRPNA LOCUS DBETHATION ACCESSION WENGOESSION KEYWOODS SOURCE ORGANISM REPERENCE AUTHORS TITLE AUTHORS TITLE JOURNAL JOURNAL JOURNAL JOURNAL JOURNAL JOURNAL	Db 529 7 0y 844 9 0y 944 9 0y 1024 8 8 0y 944 9 0y 1024 8 0y 944 9
ra" I HR" 1" ASLQIT GGMSGG PSAMMG	EMBREPHA 1068 bp DNA, 5 end of Cds. 17-MAR-1997 ETAILLA CATCOOOTS httpN gene, 5' end of Cds. 17881.1 CAL188100 httpN gene merchanterial macrotoorum. merchanterial macrotoorum. merchanterial macrotoorum. merchanterial proteoducterial pamma subdivision; Enterobacterialment of the Collaboration of the C	Trotterioscopicioscopia (1914) processo de la composicio de la composicio del consecució (1914) processo de la composicio del composicio del composicio (1914) processo de la composicio del composicio (1914) processo de la composicio del composicio (1914) processo del del composicio (1914)

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           Query Match 17.5%;
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Best Local Similarity 68.0%;
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Bauer, D. and Collimer, A.
Hypersensitive response elicitor from
Patent: US 5850015-A 6 15-DEC-1998;
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Sequence 6 from patent US
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Search completed: May 2, 2002, 04:38:12 Job time: 3727 sec Db 밁 Ş 밁 Ş 8 õ B 8 밁 S 밁 Ŷ 문 õ B õ

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Erwinia amylovora hypersensitive response

errerect

encoding DNA

AAD00668 standard; AAD00668; 08-SEP-2000 (firs

(first entry)

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		121 atcggcggtgcggaaataacgggttgctgggtaccagtcgccagaatgctgggttg 180	Db
1200 ggtggttcttcgctgggtattgatgccat	Db	atcggcggtgcggggggaataacgggttgctgggtaccagtcgccagaatgctgggttg	9
1201 ggtggttettegetgggtattgatgccat	Qy	61 gaggaatacgttatgagtctgaatacaagtgggctgggagcgtcmacgatgcmaatttct 120	Db
1141 atgatcasasggcccatggcgggtgatac	B 5	61 gaggaatacgttatgagtctgaatacaagtgggctgggagcgtcaacgatgcaaatttct 120	Qy
1081 aagccagatgacgacggaatgacaccagc	D B	1 aagetteggeatggeaegtttgacegttgggteggeaggtgaegtttgaattatteataa 60 1 aagetteggeatggeaegtttgaacegttgggteggeagggtaegtttgaatatteataa 60	B 64
1081 asgccagatgacgacggaatgacaccagc	1; 0y	; Conservative 0; Mis	×
1021 cagaaaggcccgggtcaggaggtgaaaac	Db Qy	Query Match 98.6%; Score 1269.6; DB 15; Length 1287;	B 6
961 gcgaaggaaatcggtcagttcatggacca	Db	Sequence 1287 BP; 305 A; 297 C; 431 G; 254 T; 0 other;	SS
961 gcgmäggmantcggtcagttcatggacca	Qy	bacteria.	1 88
901 ateggtacgcacaggcacagttcaacccg	Db	at the N-terminus of harpin. The 44kD protein encoded by the hrpN gene is a hypersensitive response elicitor protein. The harpin is thought to be an archetyne for HR elicitors from blytopathogenic	388
	Qy	The hrpN gene was isolated from E.amylovora using a 48-fold degenerate oligonucleotide probe corresponding to amino acids 9-15	88
841 ttaggtaacgccgtgggtaccggtatcgg	Db .	Claim 11 and Example 12; Page 27-28; 47pp; English.	* 25 X
781 ggttcgtcgctgggcggcaaagggctgcgc 841 ttaggtaacgccgtgggtatcggt	ov D	amylovora - and DNA encoding it, useful for developing harpin inhibitors to prevent e.g. fire blight of fruit	133
	ν,	Hypersensitive response elicitor protein derived from Erwinia	XX
	Db.	WPI; 1994-035054/04. P-PSDB; AAR45751.	DR DR
721 ctccttggcaacgggggactgggaggtggt	Qy	Bauer DW, Beer SV, Collmer A, He S, Laby R, Wei Z;	¥ 2 i
661 gcctataaaaaaggagtcactgatgcgctç	Db	(CORR) CORNELL RES FOUND INC.	¥ 72 3
661 gcctataaaaaaggagtcactgatgcgct	Qy	01-301-1992; 9208-0907935.	7 7 7
601 caagatggcacccagggcagttcctctgg	Db	30-JUN-1993; 93WO-US06243.	PX
601 caagatggcacccagggcagttcctctggc	Qy	20-JAN-1994.	8 \$
541 ccgatgcagcagctgctgaagatgttcagc	Db		Σ×
541 ccgatgcagcagctgctgaagatgttcagc	Qy	/transl_except= pos:11861188;aa:His /transl_except= pos:11891191;aa:Asp	FT
481 tcaacgtcccaaaacgacgattccacctcc	Qy Db	Key Location/Qualifiers	332
421 ggcggcaacaataccacttcaacaacaaat	da	Erwinia amylovora.	18
	V0	Rosaceae: apple: pear; phytopathogenic bacteria; defence reaction; hypersensitive reaction and pathogenicity; hrp; gene cluster; ds.	222
361 ggactgtogaacgctgtaacgatatgtta	nb Qy	amylovora hrpn gene.	XX
301 ggcggtggcttaggcggtggcttaggtaat	Db	11-JUL-1994 (first entry)	X D
301 ggcggtggcttaggcggtggcttaggtaat	Qy	AAQ55751;	383
241 gctggcttactcaccggcatgatgatgatg 	Oy Db	PESUIT, 8 ANG\$5751 ID ANG\$5751 standard; DNA; 1287 BP.	RESULT AAQ557
181 ggtggcaartotgcaorggggctgggcgg	Dib		
181 ggtggcaattctgcactggggctgggcggc	V V	1261 cttggcaagctgggcgcgcttaagctt 1288 1261 cttggcaagctgggcgggcttaagctt 1288 1261 cttggcaagctgggcgggcttaagctt 1288	B 5
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E 5	l ggtggttcttcggtgggtattgatgccatgatggccggtgatgccattaacaatatgca 	1201
E E	ggtgataccggcaacggcaacctgcaggcacq 	1143
8.8	asgccagatgacgacggaatgacaccagccagtatggagcagttcaacaaagccaa 	1083
= =	ccgggtcaggaggtgaaaaccgatgacaaatcatgggcaaaagcactgagc 	1021
= =	gaaggaaatoggtcagttcatggaccagtatcctgaggtgtttggcaagccgcagtac 	961
9 9	caggeacagttcaaccogttetttegteaataaaggegategggegatg 	901
9 9	ggtaccggtatcggtatgaaagcgggcattcaggcgctgaatgat 	841
0 0	ggcggcaaagggctgcaaaacctgagcgggccggtggactaccagcag	781 781
78	ggggactgggaggtggtcagggcggtaatgctggcacgggtcttgac 	721 721
7 7	aaggagtcactgatgcyctgtcgggcctgatgggtaatggtctgagccag 	661
66	ccagggcagttcctctgggggcaagcagccgaccgaaggcgagcagaac	601
60	gaagatgttcagcgagataatgcaaagcctgtttggtgatggg 	541
UI UI	caaaacgacgattccacctccggcacagattccacctcagactccagcgac 	481 481
8 8	caataccacttcaacaacaaattccccgctggaccaggc 	421 421
42	ycgctgaacgatatgttaggcggttcgctgaac&cgctgggctcgaaa 	361 361
36	aggcggtggcttaggtaatggcttgggtggctcaggtg 	301
30	tgggcggtggtgggctgatg tgggcggtggtggctgatg	241
2 2	ggtggcaattctgcactggggctgggcggtgatcaaatgataccgtcaatcagctg / 	181 181

P 64	B 8	B 8	M B Q	8 \$ 8	88888	8888	8888	PS	P X R R	X P X P	X P X F	PN WO96	X S X	222	XP	1927	Χij	RES	B 8
193 geactggggetggggggtatcaanatgatacogteaateagetggetggettactc 552 	133 99199aantamoy99ttgct9991acca9tcgcca9aatgctg99ttg99tggcaattct 192 61 99c99aantamoy9ttgct999tamogccs9aatgcty9199tg99tg9tg9tg99tg96tg96ttcc	gcaaatttctatcggcggtg gcaaatttctatcggcggtg	Query Match 89.1%; Score 1147; DB 18; Length 1159; Best Local Similarity 99.9%; Pred. No. 0; Matches 1158; Conservative 0; Hidematches 0; Indels 1; Gaps	Official Plants. Sequence 1158 BP; 280 A; 272 C; 387 G; 219 T; 0 other;	essing mbinant	contactas no tystetate. The elicitor may be used in a new method for imparting pathogen resistance to plants, by application of the elicitor in a non-infectious form to plant cells, by spraying, injection, lesi abrasion, or plant infection with recombinant	This sequence encodes a hypersensitive response elicitor from Erwinia amylovozo, with a mol.wt. of 37,000. The elicitor has a prof. 4.5, themsetability at 100 deg C for at least 10 min, and	response elicitor polypeptide or protein """ "" "" "" "" " " " " " " " " " " "	1997-051614/05. DB; AAW06598. Filing Dathogen registance to plants - with	(CORR) CORNELL RES FOUND INC. Beer SV, Wel 2;	07-JUN-1995; 95US-0475775.	W09539802-A1. 19-D80-1996.	nía amy	Hypersensitive response; elicitor; Erwinia amylovora; plant; disease-resistance; Escherichia coll; infiltration; virus; bacterium; fungus; pathogen; biological control adent; srs.	Hypersensitive response elicitor gene.	30-MAR-1997 (first entry)	AAT49314 standard; DNA; 1158 BP.	9314 9	1261 ettggcmagetgggcgcggcttmagett 1288
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RESULT AAV73507 ID AAV XX	Db Qy	B 6	Qу	Db Qy	Db Qy	D 04	B 64	D 49	8 8	8 8	P .	S B &	₽ ₽	Qy E	P 9	Db .	0 B	, VQ	D Qy
7 10 507 ANV3507 standard; DWA; 1023 BP.	1213 ctgggjaltgatggcatgg 1221 	1153 cccategorggitataccggcaarggcancticcagcagcagcgcggtcgctcttctcg 1212 1081 cccategorggitataccggcaarggcaacctgcagcagcggtcgccggttcttccg 1212 1081 cccategorgggtcataccggcaaccggcaaccgcca-gcacgcggttgcccggttgcttct 1139	1093 gerggantgacaccagccagtatggagtcaccacagccaeggcattgatcanaag 1152 	1033 gytcsgpagigaamaccyatgacaantcstgggcamagcactgagcagccogatgac 1092 961 ggtcsggaggtgammaccyatgacamatcatgggcamagcactgagcagccogatgac 1020	973 gtragitcatigaecagtatics;gagigittiggeagcocjostaccagaaaggeccg 1032 901 ggtcagitcatggaecagtatics;gagigittiggeagcocjostaccagaaaggeccg 900 901 ggtcagitcatggaecagtaticijiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	913 aggacaattcaacccgttctttcgccattaasggcgatcgggcgatggcgaaggaaatc 972	853 9t99gtacc9gtatc9gtatgaaagc9gcattcaggc9ctpaatgatatc9gtaccgcace 912	793 99990aaa9990tigcaanacctgagc999cc99tg9actaccagcagttaggtaacgcc 852		o/3 gaatcactgattgegetgtegagetgattggtaatggtetgaagetgetcettggacaac 722 [1]			aacgacgattccacctccggcacagattccacctcagactccagcgacccgatgcagcag				241 ggcggtggcttaggtaatggcttgggtggctcaggtggcctgggcgaaggactgtcgaac 300	313 99c9gt9gcttaggtaatg9cttg9gtg9ctcaggt9gcctgggcgaaggactgtcgaac 372	253 accygcatgatgatgatgatgagoatgatgygcggtygtygggttgatgygcggtygctta 312

us-09-770-693-4.rng

Thu May

23-FEB-1999 AAV73507;

07-JUN-1995; 07-JUN-1995; 15-DEC-1998

P-PSDB; Bauer D,

AAW82407 Collmer A;

1999-069852/06

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Erwinia chrysanthemi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence encodes a novel Erwinis chrysanthemi protein, http://ech.
that elicits shypersensitive response in plants. The encoding NA can be
used for imparting pathogen resistance to plants, by transforming a
plant with a wector containing the DNA and a pathogen inductible promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Column 31-34; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding Erwinia chrysanthemi hypersensitive response protein 
hrpN - useful for imparting pathogen resistance to plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1023 BP; 238 A; 254 C; 331 G; 200 T; 0 other;
                                                                                                                                                                                                                                   1085 cagatgacgacggaatgacaccagccagtatggagcagttcaacaaagccaagggcatga 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      905 gtacgcacagcacagttcaacccgttctttcgtcaataaaggcgatcgggcgatggcga 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y Match 17.5%;
Local Similarity 65.6%;
hes 328; Conservative
                                                                                                                                                                                                                                                                                                               aggamateggtemgttemtggmeemgtmtcetgmggtgttttggemmgeegemgtmeemgm 1024
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                                                                                                              tcaaaaggcccatggcgggtgataccggcaaccggcaacctgcaggcacgcggtgccggtg 1200
                                                                                                                                                                                                cggatgatgacggtatgaccggcgccagcatggacaaattccgtcaggcgatgggtatga 883
                                                                                                                                                                                                                                                                                                                                                                                                                                    aagagateggeeagtttatggateagtateeggaaatatteggtaaaceggaataceaga 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gcacccacgtagacggtaacaaccgccactttgtagataaagaagatcgcggcatggcga 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gtaatgccatcggcatgggcgtgggcagaatgctgcgctgagtgcgttgagtaacgtca 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtaacgccgtgggtaccggtatcggtatgaaagcgggcattcaggcgctgaatgatatcg 904
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gttcttcgctgggtattgatgccatgatggccggtgatgccattaacaatatggcacttg 1264
                                                                                 tcammagcgcggtggtggtacccggcmataccamcctgmacctgcgtggcgcgggcg
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Best Local Similarity 65.6
Matches 328; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides a protein (trpeEX) from Erwinia chrysnahlemi, which elicitie a hyperementitur encopones in plants. The protein may be used to produce hyperementitur encopones to plants and in its case of the produce hyperementitur encopones to plants and in the case of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1265 gcaagctgggcgcggcttaa 1284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E. chrysanthemi hypersensitive response elicitor protein ORF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E. chrysanthemi hypersensitive response elicitor protein HrpNECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Columns 9-10; 26pp; English
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     aggaaatcggtcagttcatggaccagtatcctgaggtgtttggcaagccgcagtaccaga
                                                                                                                                                                                                                                                                                                                           cttctctgggggcaggcgttgcagggcctgagcggcgcgggtgcattcaaccagttgg 583
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                                                                                             gcacccacgtagacggtaacaaccgccactttgtagataaagaagatcgcggcatggcga
                                                                                                                          gtacgcacaggcacagttcaacccgttctttcgtcaataaaggcgatcgggggatggcga
                                                                                                                                                                                                            gtaatgccatcggcatgggcgtggggcagaatgctgcgctgagtgcgttgagtaacgtca 643
                                                                                                                                                                                                                                         gtaacgccgtgggtaccggtatcggtatgaaagcgggcattcaggcgctgaatgatatcg 904
                                                                                                                                                                                                                                                                                                                                                              cgtcgctgggcggcaaagggctgcaaaacctgagcgggccggtggactaccagcagttag 844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 224.8; DB 21.
Pred. No. 1.1e-56;
0; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .8; DB 21;
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S 8 ô D Ş 망 â

704 965 644

Gaps

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1024 703 Query Match Best Local S Matches 328

785

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RESULT 12
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mils sequence encodes a hypersensitive response elicitor from 
Evrinia chypanthemic, with a early, of 34,000. The elicitor pro-
blemonetable, has a glyrade content of over 184, and has no cyteine 
prediction of the content of the contenting problem of the 
resistance to plants with a publication of the classification. Just 
infections from to plant cells, by spraying, injection, lead 
infection or plant infection with recombinant becteria (non-
intentions to the heat plant, e.g. Experición coll ) expressing 
the contention as a biological control agent, or allow recombinant be-
elition as a biological control agent, or allow recombinant on 
the contention of the content
                                                                                                                                                                                                                             Imparting pathogen resistance to plants - with hypersensitive response elicitor polypeptide or protein
                                                                                                                                                                                                                                                                                                                                                   Beer SV,
                                                                                                                                                                                                                                                                                            P-PSDB; AAW06597
                                                                                                                                                                                                                                                                                                               WPI; 1997-051614/05
                                                                                                                                                                                                                                                                                                                                                                                     (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09639802-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erwinia chrysanthemi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacterium; fungus; pathogen; biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypersensitive response; elicitor; Erwinia chrysanthemi; plant; disease resistance; Escherichia coli; infiltration; virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypersensitive response elicitor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1004 gtaagctggccaacgcctga 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1085 cagatgacgacggaatgacaccaggcagtatggagcagttcaacaaagccaagggcatga 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gcaagctgggcgcgcttaa 1284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tcaaaaggcccatggcgggtgataccggcaaccggcaacctgcaggcacgcggtgccggtg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oggatgatgacggtatgacoggcgccagcatggacaaattccgtcaggcgatgggtatga 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aaggcccgggtcaggaggtgaaaaccgatgacaaatcatgggcaaagcactgagcaagc 1084
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                                                                                                                                                                                                                                                                                                                                                   Wei
                                                                                                                                                                                            Page 45-56; 69pp; English.
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596.1618
/*tag- a
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Best Local S
Matches 328
                                                           03-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1599
                      26-FEB-1998;
                                                                                                W09837752-A1
                                                                                                                                                                                                       Erwinia chrysanthemi.
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                                                                                                                                                                                                                                            Diological
                                                                                                                                                                                                                                                                                                                                                                                                               AAV54606 standard; DNA; 2141 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtaagctggccaacgcctga 1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                        control; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                     (first entry)
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                      98WO-US03604
                                                                                                                             Location/Qualifiers
596..1618
/*tag- a
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protein infiltration into the plant. The bacterium or fungus disease-resistance on
method confers virus
crops and ornamental
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648 G; 474 T; 0 other

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Score 224.8;
Pred. No. 1.6e
0; Mismatches
. 1.6e-56;
ches 172;
                   DB 18;
indels
                 Length
                   2141;
Gaps
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gtaatgccatcggcatgggcgtggggcagaatgctgcgctgagtgcgttgagtaacgtca 1238 gtaacgccgtgggtaccggtatcggtatgaaagcgggcattcaggcgctgaatgatatcg 904 cttctctgggggcaggcggcttgcagggcctgagcggcggggtgcattcaaccagttgg 1178

gcacccacgtagacggtaacaaccgccactttgtagataaagaagatcgcggcatggcga 9tacgcacaggcacaggttcaacccgttctttcgtcaataaaggcgatcgggcgatggcga 964 1298

aggaaatcggtcagttcatggaccagtatcctgaggtgttttggcaagccgcagtaccaga 1024 aaggcccgggtcaggaggtgaaaaccgatgacaaatcatggcaaaagcactgagcaagc 1084 aagagatcggccagtttatggatcagtatccggaaatattcggtaaaccggaataccaga 1358

U99819a19acggta1gaccggccagcatggacaaa11ccgtcaggcgatgggtatga

tcaaaaggcccatggcgggtgataccggcaacgtgcaggcacgcggtgccggtg 1204 tcaaaagcgcggtggcgggtgataccggcaataccaacctgaacctgcgtggcgcggggg

1538

gtgcatcgctgggtatcgatgcggctgtcgtcggcgataaaatagccaacatgtcgctgg 9ttcttcgctgggtattgatgccatgatggccggtgatgccattaacaatatggcacttg 1264

Erwinia chrysanthemi hypersensitive response elicitor (HRE)

Hypersensitive response elicitor; HRE; insect resistance,

\$X\$CCCCCCCCCCCCXXXX

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Matches 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at his, hast stable hypersonative response elictor (NEE) (see MATSES) of Exula chyperhead. The invention relates to the use clears grown from seed treated with MEE, Also calcied is a method of inset; control for plants that involves; a) popuding a method of inset; control for plants that involves; a) popuding a method treated with MEE, also calcied is a method treated, by porting a seed treated on a recent user a MATSES. S), and (b) growing the transpent plants or transpent plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 8-9; 75pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of hypersensitive response elicitor polypeptide - for application to plants or seeds or transgenic plants or seeds for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAW75862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This DNA sequence includes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-1997;
                     1599 gtmagctggccmacgcctgm 1618
                                                                                                                                                                                                                                                                   1145 tcaaaaggcccatggcgggtgataccggcaacggcaacctgcaggcacgcggtgccggtg 1204
                                                                                                                                                                                                                                                                                                                                              1419 cggatgatgacggtatgaccggcgccagcatggacaaattccgtcaggcgatgggtatga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1179 gtaatgccatcggcatgggcgtggggcagaatgctgcgctgagtgcgttgagtaacgtca 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2141 BP; 477 A; 542 C; 648 G; 474 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            965 aggaaatcggtcagttcatggaccagtatcctgaggtgttttggcaagccgcagtaccaga 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aeggcccgggtcaggaggtgaaaeccgatgacaaatcatgggcaaaagcactgagcaagc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gtacgcacagcacagttcaacccgttctttcgtcaataaaggcgatcgggcgatggcga
                                                gcasgctgggcgcggcttaa 1284
                                                                                                                            gtgcatcgctgggtatcgatgcggctgtcgtcggcgataaaatagccaacatgtcgctgg 1598
                                                                                                                                                 gttottogotgggtattgatgocatgatggocggtgatgocattaacaatatggoacttg 1264
                                                                                                                                                                                                                                                                                                                                                                               cagatgacgacggaatgacaccagccagtatggagcagttcaacaaagccaaaggccatga 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aagagateggecagtttatggateagtateeggaaatatteggtaaaceggaataceaga 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcacccacgtagacggtaacaaccgccactttgtagataaagaacgcggcatggcga 1298
                                                                                                                                                                                                                                  tcaaaagcgcggtggcggtgataccggcaataccaacctgaacctgcgtggcgcggggcg
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Pred. No. 1.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .be-56;
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Best Local Similarity 65.6%;
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                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for enhancing plant growth - comprises use of hypersensitive response elicitor polypeptide or protein which may also effect, e.g. increase in plant height or earlier germination seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-427940/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erwinia chrysanthemi hypersensitive response elicitor (HRE) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV39972;
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                                                                                                                                       845
                                                                                                                                                                                                                  785 cgtcgctgggcggcaaagggctgcaaaacctgagcgggccggtggactaccagcagttag 844
gtacgcacaggcacagttcaacccgttctttcgtcaataaaggcgatcgggcgatggcga
                                                                                                            gtaacgccgtgggtaccggtatcggtatgaaagcgggcattcaggcgctgaatgatatcg 904
                                                                                 gtaatgccatcggcatgggcqtggggcagaatgctgcgctgagtgcgttyagtadcytca
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                                                                                                                                                                                                                                                                                                                                                                                                                                     2141 BP; 480 A; 542 C; 645 G;
                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 1.6e-56;
D; Mismatches 172; Indels
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This much outlide sequence from Envinia chrymanthemi includes a coding 
present for a 3 km hypersensitive election process (185 as ed and 
region for a 3 km hypersensitive election and the content of ever (34 and 
contains subtentially no bysteins a "My time content of ever (34 and 
sethods of impertum) hypersensitive response induced resistance to 
points by creatment of eeeds. Isolated HER polyperides can be 
upplied to seeds as a means of impertum perhapsion resistance to
                                                                                                                                                                                                                                                                         Disclosure; Page 17-18; 85pp; English
                                                                                                                                                                                                                                                                                                                                  Imparting pathogen resistance to plants - by applying hypersensitive response elicitor polypeptide to seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 785 cgtcgctgggcggcaaagggctgcaaaacctgagcgggccggtggactaccagcagttag 844
                                                  gtgcatcgctgggtatcgatgcggctgtcgtcggcgataaaatagccaacatgtcgctgg
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Title: Perfect score: Sequence:

Searched: Scoring table: Run OM nucleic

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Post-processing: Minimum Match 0%
Maximum Match 100%
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and is derived by analysis of the total score distribution.
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1: /egn2_6/podata/2/ina/Sh_coMB.seq:*
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3: /egn2_6/podata/2/ina/Sh_coMB.seq:*
4: /egn2_6/podata/2/ina/Sh_coMB.seq:*
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CITY: Rochester STATE: New York COUNTRY: U.S.A.	ochester Wew York Co.S.A.	
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APPLICATI FILING DA CLASSIFIC ATTORNEY/AC	LALAFLON DATA: CON NUMBER: US/08/200,724A XTE: 23.FEB-1994 ANTION: 530 SEMT_IMPORANTION: SENT_IMPORANTION:	
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US-09-030-270A-4
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Best Local Similarity 100
Matches 1288; Conservative
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Patent No. 5977060
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MEDIUM TYPE: TAOPPY data
COMPUTER: INAM PC COMPATILIA
SOFTWARE STREET IN PASS AND ASS
APPLICATION MEMBER: US 90/09/20, 270A
PPLICATION MEMBER: US 90/09/20, 270A
APPLICATION MEMBER: US 90/09/20
PPLICATE ON MEMBER: US 90/09/20
PP
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TELEFAX: (716) 263-1600
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
MOLECULE TYPE: DNA (get
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CORRESPONDENCE: INXOR, Bargrave, Devans & Doyle LLP
STREET: Fo. Bax 105; Clinton Square
CITY: Mochester
STREE: New York
COUNTRY: 0.5.A.

LIP: 14603.
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TELECOMMUNICATION INFORMATION:
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APPLICANT: Wei, Zhong-Min
TITLE OF INVENTION: INSECT CONTROL WITH A
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1261 cttggcaagctgggcgcgcttaagctt 1288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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REGISTRATION NUMBER: 30,727
aagCttcggcatggcacgtttgaccgttgggtcggcgtacgtttgaattattcataa 60
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I00.0%; Pred. No. 0;
Live 0; Mismatches
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LENGTH: 1288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HOLECOLE TYPE: CDNA
US-08-851-376A-3
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**TLING OME: 32-788-1984
APTOMEN/AGDET INFORMATION: 12-788-1984
APPOMEN/AGDET INFORMATION: 18-78-1984
**ENTRY AND INFORMATION: 18-78-1984
**ENTRY AND INFORMATION: 18-78-1984
**INFORMATION: 18
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Query Match 100.0%; Score 1288;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1288; Conservative 0; Mismatches
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APPLICANT: Wei, Zhong-Min
APPLICANT: Bauer, David W.
APPLICANT: Collmer, Alan
APPLICANT: He, Sheng-Yang
APPLICANT: Leby, ROn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0) Version
CURRENT APPLICATION DATA:
APPLICATION UNHEER: US/08/851,376A
FILING DATE: 05-MAY-1897
CLASSIFICATION:
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1201 ggtggttcttgctggtattgatgccatgatggcggtgatgcattaacaatatggca 1260
1201 GGTGGTTCTTCGCTGGGTATTGATGCCATGATGGCCGGTGATGCCATTAACAATATGGCA 1260
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ZIP: 14603
COMPUTER READABLE FORM
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ADDRESSEE: Nixon Peabody LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ELICITOR OF THE HYPERSENSITIVE RESPONSE TITLE OF INVENTION: IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Clinton
CITY: Rochester
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Ca 1260	cc 1200 	ige 1140 - GC 1140	igc 1080	ac 1020	atg 960	gat 900	pag 840 	gac 780 SAC 780	cag 720 AG 720	aac 660 NAC 660	999 600	gac 540 GAC 540	aac 480 AAC 480	aaa 420 AAA 420	gaa 360 GAA 360	atg 300 ATG 300	ctg 240 CTG 240	TTG 180
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Qy Db	Oy Db	ОУ	p dq	N. Be	us-o	** ** **										RES US-	Db Qy	
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181	121	61	, ,	Query Match Best Local Si Matches 1288;	US-08-984-207-4	TYPE: n STRANDED TOPOLOGY	TELEPHON INFORMATION SEQUENCE C	REGISTRA REFERENC TELECONMUN	PRIOR APPLICATE PILING D ATTORNEY/A	CURRENT APPLICATE CLASSIFI	COMPUTER COPERATIN SOFTWARE	COUNTRY: COMPUTER E	CORRESPOND STREET: CITY: F	APPLICANT TITLE OF 1 TITLE OF 1 NUMBER OF	Patent No. 63 GENERAL INFO APPLICANT APPLICANT	RESULT 4 US-08-984-207-4 ; Sequence 4, F	1261	
181	121	61	, ,	Query Match Best Local Similari Matches 1288; Cons	US-08-984-207-4	TENOTH: 1288 TYPE: nucleic STRANDEDNESS: TOPOLOGY: lin	TELEPHONE: (7 TELEPAX: (716 INFORMATION FOR SE	REGISTRATION N REFERENCE/DOCK REFERENCE/DOCK TELECOMMUNICATIO	PRIOR APPLICATION NO APPLICATION NO FILING DATE: ATTORNEY/AGENT 1	CURRINT APPLICATION NO FILING DATE: CLASSIFICATION CLASSIFICATION	MEDIUM TYPE: COMPUTER: IBM OPERATING SYST SOFTWARE: Pat	COUNTRY: U.S. ZIP: 14603 COMPUTER READABLE	CORRESPONDENCE / ADDRESSEE: N. STREET: P.O. CITY: Rochest	APLICANT: Bees TITLE OF INVENT: TITLE OF INVENT: NUMBER OF SEQUES	FALENT NO. 625974 GENERAL INFORMATIO APPLICANT: Q1u APPLICANT: We1		1261	
181	121	61	, ,	Query Match Best Local Similarity 1 Matches 1288; Conservati		: LENGTH: 1288 base; TYPE: nucleic acid STRANDEDNESS: singl TOPOLOGY: linear	* TELEPHONE: (716) 26 ** TELEPHAX: (716) 263 ** INFORMATION FOR SEQ ID 1 ** SEQUENCE CHARACTERIST	: NAME: Goldman, Micl REGISTRATION NUMBER REFERENCE, FOCKET NUM TELECOMMUNICATION INFO	PRIOR APPLICATION DATE APPLICATION NUMBER: FILING DATE: 05-DEC ATTORNEY/AGENT INFORM	: CURRENT APPLICATION DI APPLICATION NUMBER: FILING DATE: CLASSIFICATION:	MEDIUM TYPE: Flopp: COMPUTER: IBM PC CO OPERATING SYSTEM: SOFTWARE: Patentin	STATE: New York COUNTRY: U.S.A. ZIP: 14603 COMPUTER READABLE FOR	CORRESPONDENCE ADDRESS ADDRESSEE: Nixon, STREET: P.O. Box 1 CITY: Rochester	: APPLICANT: Beer, Ste : TITLE OF INVENTION: : TITLE OF INVENTION: : NUMBER OF SEQUENCES:	; Patent No. 6235974 ; GENERAL INFORMATION: ; APPLICANT: Qiu, Dewe ; APPLICANT: Wei, Zhon	RESULT 4 US-08-984-207-4 : Sequence 4, Application	1261	
181	121	61	, ,	ã		: LENGTH: 1288 base pairs : TYPE: nucleic acid : STRANDERNESS: single : TOPOLOGY: linear	: TELEPHONE: (716) 263-130 : TELEPAX: (716) 263-1600 : INFORMATION FOR SEQ ID NO: 4 : SEQUENCE CHARACTERISTICS:	NAME: GOLDMAN, Michael L REGISTRATION NUMBER: 30,0 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATI	PRIOR APPLICATION DATA: APPLICATION NUMBER: US 6 FILING DATE: US-DEC-1996 ATTORNEY/AGENT INFORMATION:	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/O FILING DATE: CLASSIFICATION:	: MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compati ; OPERNATING SYSTEM: PC-DOS ; SOFTWARE: Patentin Relea	STATE: New York COUNTRY: U.S.A. ZIP: 14603 COMPUTER READABLE FORM:	CORRESPONDENCE ADDRESS: ADDRESSEE: Nixon, Hargra STREET: P.O. Box 1051, C	APPLICANT: Beer, Steven V. TITLE OF INVENTION: HYPERS TITLE OF INVENTION: RESIST NUMBER OF SEQUENCES: 10	; PALENT NO. 6235974 ; GENERAL INFORMATION: ; APPLICANT: Qiu, Dewen ; APPLICANT: Wei, Zhong-Min	RESULT 4 US-08-984-207-4 ; Sequence 4, Application US/089	1261	
181	121	61	, ,	100.0%; 100.0%; /ative 0	: MOLECULE TYPE: DNA (genomic) US-08-984-207-4	: LENGTH: 1288 base pairs) TYPE: nucleic acid STRANDENNESS: single TOPOLOGY: linear	*ELEPHONE: (716) 263-1304 *TELEPAX: (716) 263-1600 *INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:		PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/033, FILING DATE: 05-DEC-1996 ATTORNEY/AGENT INFORMATION:	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/984, FILING DATE: CLASSIFICATION:	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible DERMYING SYSTEM: PC-DOS/MS-DC SOFTWARE: Patentin Release #1	STATE: New York COUNTRY: U.S.A. ZIP: 14603 COMPUTER READABLE FORM:	CORRESPONDENCE ADDRESS: ADDRESSEE: Mixon, Hargrave, Dusceller P.O. Box 1051, Clinton CITY: Rochester	APPLICANT: Beer, Steven V. TITLE OF INVENTION: HYPERSENSIT TITLE OF INVENTION: RESISTANCE UNMER OF SEQUENCES: 10	Patent No. 6235974 GENERAL INFORMATION: APPLICANT: Qiu. Dewen APPLICANT: Wei, Zhong-Min	RESULT 4 US-08-984-207-4 : Sequence 4, Application US/08984207	1261	
181	121	61	, ,	100.0%; 100.0%; /ative 0		: LENGTH: 1288 base pairs : TYPE: nucleic acid : STRANDEDNESS: single : TOPOLOGY: linear	TELEPHONE: (716) 263-1304 TELEPAX: (716) 263-1600 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:	: NAME: Goldman, Micheel L. REGISTRATION NUMBER: 30,727 REFERENCE/DOCKET NUMBER: 19603/1201 TELECOMMUNICATION INFORMATION:	PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/033,230 FILING DATE: 05-DEC-1996 ATTORNEY/AGENT INFORMATION:	8/984,20	ble 7MS-DOS se #1.0,	STATE: New York COUNTRY: U.S.A. ZIP: 14603 COMPUTER READABLE FORM:	CORRESPONDENCE ADDRESS: ADDRESSEE: Nixon, Hargrave, Devans . STREET: P.O. Box 1051, Clinton Squa: CITY: Rochester	: APPLICAMT: Beer, Steven V. : TITLE OF INVENTION: HYPERSENSITIVE RE : TITLE OF INVENTION: RESISTANCE IN FLA : NUMBER OF SEQUENCES: 10	; PATENT NO. 6235974 ; GENERAL INFORMATION: ; APPLICANT: Qiu, Deven ; APPLICANT: Wei, Zhong-Min	RESULT 4 US-08-984-207-4 : Sequence 4, Application US/08984207	1261	
181	121	61	, ,	100.0%; Score 1288; 100.0%; Pred. No. 0; vative 0; Mismatches		LENGTH: 1288 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	ELEPHONE: (716) 263-1304 TELEPAN: (716) 263-1500 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:		PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/033,230 FILING DATE: 05-D8C-1996 ATTORNEY/AGENT INDORNATION:	8/984,20	ble 7MS-DOS se #1.0,	STATE: New York COUNTRY: U.S.A. ; COUNTRY: U.S.A. ; COMPUTER REALANDLE FORM:	: CORRESPONDENCE ADDRESS: ADDRESSEE: Nixon, Hargrave, Devans & Doyl STREET: P.O. Box 1051, Clinton Square CITY: Rochester	APPLICAMY: Beer, Steven V. TITLE OF INVENTION: HYPERSENSITIVE RESPONSE TITLE OF INVENTION: RESISTANCE IN PLANTS BY NUMBER OF SEQUENCES: 10	PATENT NO. 6255974 GENERAL INFORMATION: APPLICANT: Qiu, Dewen APPLICANT: Wei, Zhong-Min	RESULT 4. US-08-904-207-4. US-08-904-207-4. Application US/08984207	1261 cttggcagctgggggggggttaagctt	
181	121	61	, ,	100.0%; Score 1288; DB 4; 100.0%; Pred. No. 0; vative 0; Mismatches 0;		: LENGTH: 1288 base pairs TYPE: nucleic ocid : STRANDEDWESS: single : TOPOLOGY: linear	TELEPHONE: (716) 263-1304 TELEPHA: (716) 263-1400 TELEPHA: (716) 263-1400 SEQUENCE CHARACTERISTICS:		: PRIOR APPLICATION DATA: : APPLICATION UNITA: US 60/033,230 : ETILING DATE: US 60/033,230 : ATTORNEY,AGENT INFORMATION:	8/984,20	MEDIUM TWEE: Floppy disk COMPUTER: HM PC COMPUTED: COMPUTER: HM PC COS/MS-DOS PERMATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Batenith Release #1.0, Version #1.30	SYNTE: New York COUNTRY: U.S.A. ZIP: 14603 CONFUTER REMANSLE FORM:	CORRESPONDENCE ADDRESS: ADDRESSE: Nixon Hargrave, Devans & Doyle LLP STREET: P.O. Box 1051, Clinton Square CITY: Rochester : CITY: Rochester	SENSITIVE RESPONSE	Patent No. 6335974 GENERAL INFORMATION APPLICANT: Q1i, Deven APPLICANT: Wel. Zhong-Min	RESULT 10-10-10-10-10-10-10-10-10-10-10-10-10-1	1261	
181	121	61	, ,	100.0%; Score 1288; DB 4; 100.0%; Pred. No. 0; vative 0; Mismatches 0;		LINGTH: 1288 base pairs TYPE: nucleic ocid STRANDEDNESS: single 'OPOLOGY: linear	TELEPHONE: (716) 263-1304 TELEPHONE: (716) 263-1600 INFORMATION FOR ESD ID NO: 4: SEQUENCE CHARACTERISTICS:		PRIOR APPLICATION DATA: APPLICATION WINER: US 60/033,230 FILING DATE: 05-DBC-1996 ATTORNEY,AGENT INFORMATION:	8/984,20	ble 7MS-DOS se #1.0,	STATE: New York COUNTRY: U.S.A. I.E. 14603 COMPUTER REMANALE FORM:	rgrave, Devans & Doyle 1, Clinton Square	SENSITIVE RESPONSE	Patent No. 6235974 CEMERAL INFORMATION: APPLICANT: Olfu, Deven APPLICANT: Nel. Zhong-Hin	RESULT 4 US-08-98-4207-4 : Sequence 4, Application US/08984207	1261	
181	121	61	, ,	100.0%; Score 1288; DB 4; 100.0%; Pred. No. 0; vative 0; Mismatches 0;		LENOTH: 1288 base pairs TYPE: nucleic odd i STANDENNESS: single TOPOLOSY: linear	TELEPHONE: (716) 263-1304 TELEPHONE: (716) 263-1600 INFORMATION FOR SED ID NO: 4: SEQUENCE CHARACTERISTICS:		PRICER APPLICATION DATA: PRICER APPLICATION NUMBER: US 60/033,230 PRILING DATE: 05-DEC-196 PRICER SAMPTINON/MATON:	8/984,20	ble 7MS-DOS se #1.0,	STATE: New York COUNTRY: U.S.A. COUNTRY: U.S.A	rgrave, Devans & Doyle 1, Clinton Square	BENSITIVE RESPONSE	Patent No. 6335974 GENERAL INFORMATION: APPLICANT Oil Down In APPLICANT Mel. Mel. Zhong-Min	RESULT - 007-94 - 207-4	1261	
				100.0%; Score 1288; DB 4; Length 128 100.0%; Pred. No. 0; Wative 0; Mismatches 0; Indels		LENGTH: 1288 base pairs TYPE: nucleic acid STANUDDNESS: single TOPOLOGY: linear	TELEPHONE: (716) 263-1204 TELEPHONE: (716) 263-1600 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CLIRACTERISTICS:		PRIOR REPLICATION DATA: APPLICATION NUMBER: US 60/033,230 FILING DATE: 05-DEC-1996 ATTONNEY/AREP/INFORMATION:	8/984,20	ble 7MS-DOS se #1.0,	STATE: New York COUNTRY: U.S.A. COUNTRY: U.S.A. CXIP: 14603 CXPTER REALABLE FORM:	rgrave, Devans & Doyle 1, Clinton Square	SENSITIVE RESPONSE	Patent No. 62397/4 GENERAL TREPSPANTON: GENERAL TREPSPANTON: APPLICANE: QLu. Deven APPLICANE: AGI. Zhong-Min	RESULT 4 UNS-08-984-207-4 15 Sequence 4 Application US/08984207	1261	Db 1201 GGTGGTTCTTCGCTGGGTATTGATGCCATGATGGCCGGTGATGCCATTAACAATATGGCA 1260

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181 ggragcant criscactaggstiggsggsggtantcanaatgatacogtcantcagetig 240
181 ggragcantrotactactaggsctiggsccsscsstantcanaatgataccsccattantcagetig 240 121 alcogcogicogogogoaataacoggiteceggitaccogicogcoagaalqotoggitty 180
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121 alcogcogicogogogoaataacoggitoccoggitacogcogcoagaangocoggitacoggitacoggitacog

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301 ggcggtggcttaggcggtggcttaggttaatggcttgggtggctcaggtggcctgggcgaa 360 241 GCTGGCTTACTCACCGGCATGATGATGATGATGATGATGATGGGCSGTGGTGGGCTGATG 밁

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US-09-013-587-4
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; MOLECULE TYPE: DNA (genomic)
US-09-013-587-4
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RODIESTO, MUNIERI SO, 727
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Patent No. 6277814
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1288; Conservative 0; Mismatches
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TITLE OF INVENTO: EMHANCEMENT OF GROWTH IN PLANTS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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COMPUTER: IR MY COMPALTHE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: DETECTLE RE-BEASE #1.0, VETSION #1.30
CURRENT APPLICATION DATA:
OPERATION OF A TOP OF THE STATEMENT APPLICATION DATA:
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APPLICATION NUMBER: US 6:
FILING DATE: 27-JAN-1997
ATTORNEY/AGENT INFORMATION:
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APPLICANT: Wei, Zhong-Min
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STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
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TRY: U.S.A.
14603
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PERT-US93-06243-3
SEQUENCE 3. Application PC/TUS9306243
SEQUENCE 3. APPLICANT: Disory Min Wei, David M. Bauer, Steven V. APPLICANT: Deer, Alan Collmer, Sheng-Yang He, and Ron
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PCT-US93-06243-3
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REGISTARION NUMBER: 26 824
REGISTARION NUMBER: CRE
TELECOMMULICATION IN COMMUNICATION:
TELECHONE: (203)268-1951
TELECHONE: (201)268-1951
INFORMATION 1008-8000 D NO. 3:
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COUNTRY: OSSILA.

COUNT
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LENGTH: 1287 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
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ATTORNEY/AGENT INFORMATION:
NAME: GOldman, Michael I
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MEDIUM TYPE: Floppy disk
COMPUTER: ITM PC Compatible
COMPUTER: ITM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,724A
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P õ D 8

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APPLICANT: Best Seven V.
APPLICANT: Bollow: Alan
APPLICANT: Bollow: Alan
APPLICANT: Bollow: Alan
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Title OF IMPRITION: BLICTION OF FT
TITLE OF IMPRITION: BLICTION OF FT
MUMBER OF SEQUENCES: V.
NOMER OF SEQUENCES: V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08851376A
Patent No. 6174717
                                                                                                                                                                     ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Rochester
STATE: NY
COUNTRY: U.S.A.
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1209; Conservative 0; Mismatches
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REFERENCE/DOCKET NUMBER: 19603/10035
TELECOMPINICATION INVOMMATION:
TELECHONE: (716) 563-1500
TELECHON: (716) 563-1500
SEQUENCE: CHANCIELISTICS:
SEQUENCE: CHANCIELISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/A
APPLICATION USER: US-MAY-199:
CLASSIFICATION:
PRIOR APPLICATION DATA:
        613
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FILING DATE: 23-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: GOLDMAN, Michael L.
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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DB 4; Length 1209; Indels 0;

Gaps

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252

ACCGGCATGATGATGATGATGAGCATGATGGGCGGTGGTGGGCTGATGGGCGTGGCTTA 240

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CAGGGCAGTTCCTCTGGGGGCAAGCGAAGCGAAGGCGAAGACGCCTNTAAAAAA 600

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US-08-891-254-4
                                                                                                                                                                                                                                                               Patent No. 5776889
                        GENERAL INFORMATION
                                                                                                                                                                           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                   APPLICANT: Wei, Zhong-Min
APPLICANT: Beer, Steven V.
TITLE OF INVENTION: Hypersensitive Response
TITLE OF INVENTION: Induced Resistance In Plants
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                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                  STREET: Clinton
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
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Best Local Similarity 99.9%;
Matches 1158; Conservative
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TELEPHONE: (716) 263-1304
TELEPAX: (716) 263-1500
INFORMATION FOR SED ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
8-891-254-4
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LENGTH: 1158 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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acactteameanattclcagctggacaggggtggtattmactcamegtccam
accacttcameanattclccgctggacagggctgggtattmactcnacgtccam
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                                                                        9999act99a9t99tea99c99teatcttacegtcae99tcttacegtcectg
                                                                                                             ACCGCCATGATGATGATGAGCATGATGGGCGGTGGTGGGCTGATGGGCGGTGGCTTA
GTGGGTACCGGTATCGGTATGAAAGCGGGCATTCAGGCGCTGAATGATATCGGTACGCAC
         gtgggtaccggtatcggtatgaaagcgggcattcaggcgctgaatgatatcggtacgcac
                                     GGCGGCAAAGGGCTGCAAAACCTGAGCGGGCCGGTGGACTACCAGCAGTTAGGTAACGCC
                                            ggcggcaaagggctgcaaaacctgagcgggccggtggactaccagcagttaggtaacgcc 852
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Pred. No. 0;
0; Mismatches
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US-08-819-539-4
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                                                                                                       Sequence 4. Application US/08819839
Patent No. 585032 A
Patent No. 585032 A
APPLICANT: Mol. Zhong-Min
APPLICANT APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLICANT-APPLIC
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/819,539
FILING DATE: 17-HAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/475,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
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                         DNA (genomic)
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Query Match

89.1%; Score 1147; DB 2; Length 1158;

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P OY DD DD WAR	est Loca atches 1 73 a 1 A 133 g 133 g 193 g 193 g 193 g 193 g 194 G	It Coal Smillarity 99.9%, Pred. No. 0: Total Smillarity 99.9%, Pred. No. 9%, Pred. No. 0: Total Smillarity 99.9%, Pred. No. 9%,
8 8	313	99995490tta99taat99ctt9995495tca995499cct99959aa9aac45tc99ac 372
8 8 8	373 301 433	Opentealegatatititagesgittegtegaaaaggtigggttgaaagggggaaaaat 432
8 % 8	493	A-UNCTITUDALINALINALINALINCUCQGTTGGGCAGGGGTATTAACTCAACGTCCCAA 420 acqaeqattccaacctccggacagasttccaacctcagactccagcgacccastscaacagas
8 5	553 481	CTGCTERAGATGTTCAGCGAGATATAGCGAGAGCCTGTLTGGTGAGGGCAGGATGGGCAGCC 612
8 8	613 541	Caggosagttoctotggggcaagcagcogaccgaaggcgagcagaagcctataaaaaa 672
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Qr 133 poettegigetagegegetatakananspatasoptomiosperigetegetatete 232 Db 121 CHILITATION INTERNATIONAL CONTRACTOR CON	Qy 133 ggcggaaataacgggttgctggtggtaccagtcgccagaatgctgggttgggtggcaattct 192 p [[1] [[1] [[1] [[1] [[1] [[1] [[1] [[1]	casytyggctyggagogtcaacgatycaaatttctatcygcygtygcy 132 	Ouery Match 99.1%; Score 1147; DB 5; Length 1158; Best Local Saninarity 99.9%; Prod. No. 0; D 5; Length 1158; Best Local Saninarity 99.9%; Prod. No. 0; Indels 1; Gaps 1;	STRANDEDNESS: single TOPOLOGY: linear TO	INFORMATION FOR ESQ ID NO: 4: SEQUENCE CHANCYBRASTICS: LENGTH: 1158 base pairs FYPE: naciata cald.rs	TREEDROMES (JULKARI MADRINE: 1900-JANO) TREEDROMES (JULKARI) TREEDROMES (JULKARI) TREEDROMES (JULKARI) TREEDROMES (JULKARI) TREEDROMES (JULKARI)	FILING DATE: VV-JUN-1995 ATTONNEY/AGRET HEODARTON: NAME: GGLEMEN, NICHAEL II. REGISTRATION HUMBER: 30/727	FILING DATE: CLASSIFICATION PRIDE APPLICATION MARA: APPLICATION MODER: US 08/475,775	CHERNTING SYSTEM: PC-U-DAYMS-U-DAS SOPTHARES: Petentin Release #1.0, Version #1.30 CHERNT APPLICATION DURYN: PCT/US96/08819 APPLICATION NUMBER: PCT/US96/08819	COMPUTER RADABALE FORM: MEDIUM TIPE: Floppy disk COMPUTER RETE I THE FC COMPUTER RADABALE FORMS FOR FREE FLORE FOR FREE FOR FREE FREE FREE FREE FRE	STREET: CLINION SQUARE, P.O. BOA AVOA CITY: Rochester STATE: New York COUNTRY: U.S.A.	TITLE OF INVENTION: RESISTANCE IN PLANTS NUMBERS OF SEQUENCES: OF SECUENCES OF SECU		RESULT 11 PCT-USS6-08819-4	Oy 1213 ctgggtattgatggcatga 1231 bb 1140 CtggatattGattgattgat 158	Oy 1153 cccatagoggstgatacoggcaacgcaacgcaaggaaggaaggaggaggaggaggtgacggtgatttag 20 111111111111111111111111111111111111	Db 1021 GACGGAATGACCAGCCAGTATGGAGCAGTTCAACAAAGGCCAAGGGCATGATCAAAAGG 1080
RESULT 12 POT USB3-0643-4 Sequence 4, Application PC/TUS9106243 Sequence 4, Application PC/TUS9106243 SERVICAN DAMON MAN No. 1, April M. Maner, Steven V. APPLICANT: Beer, Alan Collmer, Sheng-Yang Ne, and Ron J. Laby	Db 1140 CTGGGTATTGATGCATCA 1158	1081	Oy 103 spospastycaccasccsctattsgasgosgiticaacaasgicaasgigsatgiticaaaasgi Oy 103 spospastycaccasccasccattsgasgosgiticaacaasgi Oya 103 spospastycaccasccasccascascascascascascascascasca	Oy 1033 ggtcogeoggtganancegatgacaantentegggcanangeatgaagcaagcaggtgac Db 961 GETCAGGAGGTGAAAACCGATGACAATTACGGCCAAAACCCAGAGCAGGCCAGATGAC	Oy 973 igitosgittostiganosgiaktocigajagistitiggaajgoogaajacotagaaajgoog Db 901 GGTCAGTICANGAACAGNATOCTGAGGTGTTTGGCAAGGCCCAGTACCAGAAMGGCCCC Db 901 GGTCAGTICANGAACAGNATOCTGAGGTGTTTGGCAAGGCCCAGTACCAGAAMGGCCCC	Oy 913 aggonosyttcas-cogitetteg-cost-sasgegateggggas-ggasasgasateggg-cost-ggggas-ggasasgasateggggas-ggggsasgasgasgasgasgasgasgasgasgasgasgas	Qy 853 graggiancegitatcegitatepaangcagganttcaggcsctagatatcggtancegtagganttcagganttcaggcattcaggcattcagganttcagg	QY 793 ggcsgcanaggctgoanancripagcsgcsgcsgcsgcacaccagacttagirancric Db 721 ggcsgcanaggstgoanancripagcsgcsgcsgcsgcacaccagacttagirancric Db 721 ggcsgcanaggstgoanancripagcagaccagactagirancrincing	Oy 733 ggggertggeograficaggergstaatgetggeracggertgggergg 13 ggggertggeograficaggerggerggerggerggerggerggerggerggergge	Oy 673 gasqtrontpaktogciqtroggoctgataggtaatggtctgacoggtccttggcaac Db 601 GGAGTCACTGATGCGCTGTCGGGCCTGATGGGTAATGGTCTGAGCCAGCTCTTGGCAAC	Qy 613 cangapantroctic:gggggcangcagacagacagacagacagacatalaanaana	Oy 553 ct.gctpa.agt.gt.cac/gapt.ast.gcapacast.gt.ca/gapt.gapt.agt.gapt.gapt.agt.gapt.gapt.agt.gapt.gap	QY 43 aacjacpattconcticograeapattcoacctcapattcoacctapatcoaccapaccoatgoagear Db 421 AACGACGATTCCACCTCCGGCACAGATTCCACCTCAGACTCCAGCGACCGGATGCAGCAG	Qy 43 accentraceanceantrocogregaceagogregagratus (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	Oy 373 gogctgaecgntstyttaggegyttegctgaecogsttggctcgaeaggeggcaecast	Oy 313 9909959Cttba99tants9ctts9959ctca99fcts9959ca990ct9fc9aa	Db 181 ACCGGCATGATGATGATGATGAGGATGGGCGGTGGTGGGCTGATGGGCGGTGGCTTA

1139	CCCATGGCGGGTGATACCGGCAACGGCAACCTGCA-GCACGCGGTGCCGGTGGTTCTTC	1081	Db
1212	cccatggcgggtgataccggcaacggcaacctgcaggcacgcc	put.	Qy
1080	CGGAATGACACCAGCCAGTATGGAGCAGTTCAACAAAGCCAAGGGCATGATCAAAAG	1021	Db
1152	gacggaatgacaccagccagtatggagcagttcaacaagccaagggcatgatcaaaagg	1093	Qy
1020	TCAGGAGGTGAAAACCGATGACAAATCATTGGGCAAAAAGCACTGAGCAAGCCAGATGAC	961	Db
1092	gtcaggaggtgaaaaccgatgacaaatcatgggcaaaagcactgagcaaggccagatgac	1033	9
960	TCAGTTCATGGACCAGTATCCTGAGGTGTTTGGCAAGCCGCAGTACCAGAAAAGGCCCG	901	B
1032	ggtcagttcatggaccagtatcctgaggtgtttggcaagccgcagtaccagaaaggcccg	973	Qy
900	AGGCACAGTTCAACCCGTTCTTTCGTCAATAAAGGCGATCGGGCGATGGCGAAGGAAATC	841	В
972	aggcacagttcaacccgttctttcgtcaataaaggcgatcgggcgatggcgaaggaaatc	913	9
840	GTGGGTACCGGTATCGGTATGAAAGCGGGCATTCAGGCGCTGAATGATATCGGTACGCAC	781	В
912	gtgggtaccggtatcggtatgaaagcgggcattcaggcgctgaatgatatcggtacgcac	853	9
780	GCCGCAAAGGGCTGCAAAACCTGAGCGGGCGGTGGACTACCAGCAGTTAGGTAACGCC	721	Db
852	aaagggctgcaaaacctgagcgggccggtggactaccagcagttaggtaacgcc	793	Qy
720	GACGGTTCGTCGCTG	661	Db
792	ggggactgggaggtggtcagggtgatatgctggcacgggtcttgacggttcgctg	733	0y
660	GTCACTGATGCGCTGTCGGGCCTGATGGGTAATGGTCTGAGCCAGCTCCTTGGCAAC	601	Db
732	agtcactgatgcgctgtcgggcctgatgggtaatggtctgagccagctcctttggcaac	673	φ
600	CCGAAGGCGAGCAGAACGCCTATAAAAAA	541	Db
672	agggcagttcctctgggggcaagcagaccgaccgaaggcggagcagaacgcctataaaaaa	613	Qy
540	NTAATGCAAAGCCTGTTTGGTGATGGGCAAGATGGCACC	481	Db
612	tgctgaagatgttcagcgagataatgcaaagcctgtttggtgatgggcaagatggcacc	553	Qy
480	GACGATTCCACCTCCGGCACAGATTCCACCTCAGACTCCAGCGACCCGATGCAGCAG	421	DЪ
552	aacgacgattccacctccggcacagattccacctcagactccagcgacccgatgcagcag	493	9
420	TTCAACAACTTCCCCCCTGGACCAGGCGCTGGGTATTAACTCAACGTCCGAA	361	Db
492	cacttcaacaacaattoccogotggaccaggcgctgggtattaactcaacgtcccaa	433	Qy
360	PAGGCGGTTCGCTGAACACGCTGGGCTCGAAAGGCGGCAACAAT	301	Db
432	cgctgaacgatatgttaggcggttcgctgaacacgctgggctcgaaaggcggcaacaat	373	Qy
300	TGGGCGAAGGACTGTCGAAC	241	Db
372	gcggtggcttaggtaatggcttgggtggctcaggtggcctgggcgaaggactgtcgaac	313	Qy
240	ACCGCCATGATGATGATGATGAGCATGATGGCCGGTGGTGGGCGGTGGCTTA 1	181	Db

19	Oberty Match Sest Local Stallarity 98.64; Score 1140.6; DB 5; Length 1159; Best Local Stallarity 99.64; Fred. Mc.) Matches 1154; Conservative 0; Mainstches 4; Indals 1; Caps 1; 77 adjactional conservative 0; Mainstches 127 77 adjactional conservative 0; Mainstches 128 71 adjactional conservative 0	APPLICATION INNOBES: 907.935 PELINO DATE: 0.3UL-1925 PELINO DATE: 0.3UL-1925 PELINO DATE: 0.3UL-1925 NAME: 0.5UL-1925 PELINOSE: 0.5UL-192	TITLE OF INVESTION. Elicitor of the Hypersensitive Response in Plants INVEST. OF SECURIORIS: 5 CHEERS OF SECURIORIS: 4 STREET: JA SHOOD ELVE STREET: JA SHOOD ELVE STREET: JA SHOOD ELVE STREET: JA SHOOD ELVE CHEER: JA SHOOD ELVE JELLOUE JA JA SHOOD ELVE JELLOUE JA
RISUIT 135 - 6 US-08-44-35-6 Sequence 5. Mpillcation US/08484318 Sequence 5. Mpillcation US/08484318 Sequence 6. Mpillcation GENERAL IMPROPRIETION: APPLICANT: Baner, waid APPLICANT: Maner, waid APPLICANT: Maner, waid TITLE 0F INVENTION: From TITLE 0F INVENTION: From TITLE 0F INVENTION: From ADMISSISS: ADMISSISS: ALMON, INTERIOVE, Davans & Doyle STREET: Clinton Square STATE: Base Vote STATE	Oy 103 graphic processors to the processor of the process	721 853 781 913 841 973 901	OY 55 ctortonomications/popularian-technologistic togglophologistic togglophologisti

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                                                                                                                                                                               US-09-118-959-6
                                                                                                                    Sequence 6, Application US/09118959
Patent No. 6001959
GENERAL INFORMATION:
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Best Local Similarity 65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 716-263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
MPLICANT: Bauer, bavid
APPLICANT: Coller, Alan
TITLE OF INVENTION: Expersensitive Response Elicitor From
TITLE OF INVENTION: Evania Chrysanthem1
NUMBER OF ISOQUENCES: 6
COMMESSOURNES: 6
COMMESSOURNES: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1145 tcasasggcccatggcgggtgataccggcaacggcaacctgcaggcacgcggtgccggtg 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1025 aaggcccgggtcaggaggtgaaaaccgatgacaaatcatgggcaaaagcactgagcaagc 1084
                                                                                                                                                                                                                                                         1004 GTAAGCTGGCCAACGCCTGA 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     764 AAGATGGCTGGAGTTCGCCGAAGACGGACGACAAATCCTGGGCTAAAGCGCTGAGTAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGAGATCGGCCAGTTTATGGATCAGTATCCGGAAATATTCGGTAAACCGGAATACCAGA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aggamatcggtcagttcatggaccagtatcctgaggtgtttggcamgccgcagtaccaga 1024
                                                                                                                                                                                                                                                                                gcaagctgggcgcggcttaa 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACCCACGTAGACGGTAACAACCGCCACTTTGTAGATAAAGAAGATEGCGGCATGGCGA 703
                                                                                                                                                                                                                                                                                                                                                                                                                 TCAAAAGCGCGGTGGCGGGTGATACCGGCAATACCAACCTGAACCTGCGTGGCGCGGGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 224.8; DB 2;
pred. No. 9.2e-58;
0; Mismatches 172;
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TELEPHONE: 716-26-21-1600
INFORMATION FOR SED ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.5%;
Best Local Similarity 65.6%;
Matches 328; Conservative
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COMPUTER READABLE FORM:
KEDIUM TYPE: Floppy disk
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-1058/MS-DOS
SOFTMARE: PROCEITIN Release $1.0, Version $1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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TELEPHONE: 716-263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     785 cgtcgctgggcggcaaagggctgcaaaacctgagcgggccggttggactaccagcagttag 844
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                                                                                                                               884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584 GTAATGCCATCGGCATGGGCGTGGGGCAGAATGCTGCGCTGAGTGCGTTGAGTAACGTCA 64:
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CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Nixon, Hargrave, Devans & Doyle
gcaagctgggcgcgccttaa 1280
                                                    GTGCATCGCTGGGTATCGATGCGGCTGTCGTCGGCGATAAAATAGCCAACATGTCGCTGG
                                                                              gttcttcgctgggtattgatgccatgatggccggtgatgccattaacaatatggcacttg 1284
                                                                                                                               TCANAGCGCGGTGGCGGGTGATACCGGCAATACCAACCTGAACCTGCGTGGCGCGGGGG
                                                                                                                                                  toaaaaggcccatggcgggtgataccggcaacggcaacctgcaggcacgcggtgccggtg 1204
                                                                                                                                                                                                          CGGATGATGACGGTATGACCGGCGCCAGCATGGACAAATTCCGTCAGGCGATGGGTATGA
                                                                                                                                                                                                                             cagatgacgacggaatgacaccagccagtatggagcagttcaacaaagccaagggcatga
                                                                                                                                                                                                                                                                              AGATGCCTGGAGTTCGCCGAAGACGGACGACAATCCTGGGCTAAAGCGCTGAGTAAAC
                                                                                                                                                                                                                                                                                                    aaggcccgggtcaggaggtgaaaaccgatgacaaatcatgggcaaaagcactgagcaagc
                                                                                                                                                                                                                                                                                                                                                         AAGAGATCGGCCAGTTTATGGATCAGTATCCGGAAATATTCCGGTAAACCGGAATACCAGA
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Pred. No. 9.2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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; MOLECULE TYPE: DNA (genomic)
US-08-891-254-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: GOLIMAN, MIChael L.

BEGISTHATURE NOMER: 0.727

BEGISTHATURE NOMER: 14637/1050

TRIACOMMUNICATION NOMER: 10437/1050

TRIACOMMUNICATION NOMER: 10437/1050

TRIACOMMUNICATION NOMER: 10437/1050

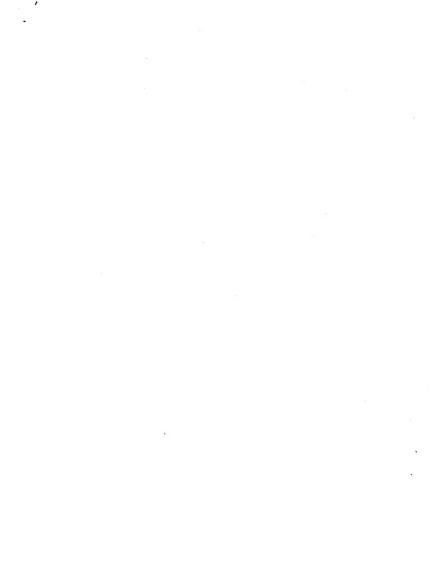
INDUSTRIAL SEGUE NO. 2:

BEGINNER: CHARACTERISTICS:

BEGUNER: CHARACTERISTICS:
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Patent No. 5776889
GENERAL INFORMATION:
108 csgartgacsgacsgaatgacsaccasgcosgtatggagcsgttcascosasgccasgcastga 1144
1019 csgartgacsgacsgaatgacsaccasgcosgtatgasgcsgttcascosasgccasgcasgcatga 1144
1011 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111
                                                                                                                                                                                                                                                            1359 AAGATGGCTGGAGTTCGCCGAAAGACGGACGACAAATCCTGGGCTAAAGCGCTGAGTAAAC 1418
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,775
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TITLE OF INVENTION: Induced Resistance In Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wei, Zhong-Min
APPLICANT: Beer, Steven V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    845 gtaxogocgtgggtacoggtatoggtatgaaagogggcattcaggcgctgaatgatatcg 904
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Clinton Square, P.O. Box 1051
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Search completed: May 2, 2002, 04:06:02 Job time: 1812 sec



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C 1 45.6 3.5 1280 11 RF66239 RF662439 SPE62439 SPE62430 SPE62439 S	SUMMARIES Ph Length DB ID Description	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	14: eargist, fun: 15: eargist, fun: 16: eargist, fun: 17: eargist, fun: 18: eargist,	4 em.escon* 5 em.escon* 7 em.escyl* 8 em.escyl* 9 em.escyl* 10 em.escyl* 11 ob.escl* 11 ob.escl* 11 ob.escl*	Database: 1 EST:	Post-processing: Minimum Match (% Maximum Match 100% Maximum Maxim	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Total number of hits satisfying chosen parameters: 22703874	Searched: 11351937 seqs, 5372889281 residues	Scoring table: IDENTITY_NUC Gapon 10.0 , Gapext 1.0	Title: US-09-770-693-4 Perfect score: 1288 Sequence: 1 asgcttoggcntsgconcgitgctgggcgcggcttasgctt 1288	Run on: May 2, 2002, 03:35:10; Search time 1557.02 Seconds [Note of the search time 1557.02 Seconds will be seen that 1557.02 Seconds will be	OM nucleic - nucleic search, using sw model	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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e 1L00 " by Jorganism="Chlamydomonas reinhardtii" jstrain="Cc-1650 wild type mt+ 2lgr" jby.xrei="taxon:3055" jby.xrei="taxon:3055" reinhardtii cc-1690, Stress condition I,	source
	ATURES
Email: chauser@duke.edu.	
Tel: 919 613 8159	
Durham, NC 27708-1000	
DCMB Box 91000	
Contact: Charles Hauser	MENT
Vascular Plants; project phase 3	
Analyses of the Chlamydomonas reinhardtii Genome: A Model,	FITLE
<pre>Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.</pre>	AUTHORS
1 (bases 1 to 1280)	PERENCE
Chlamydomonadaceae; Chlamydomonas.	
Chlamydomonas reinhardtii	DRGANISM
Chlamydomonas reinhardtii.	JRCE
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BF864339 1280 bp mRNA EST 19-JAN-2001	SUS
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normalized, Lambda Zap III | SK-; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey XhoI;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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McDermott,J.P., Sliflow.C., Stern.D. and Surzyckl.R.
Analyses of the Chiamydomas reinhardtil Genome: A wedel,
Unicellular System for Analyzing Gene Punction and Regulation in
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DCMB Box 91000
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Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 568)
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1024075A04.yl C. reinhardtii CC-1690, normaliz
Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Motoe-Wector: paluescript II SY: Site_1: scoti; Site_2: abzil: This liberary constructed by oith nowless and setting abzil: This liberary constructed by oith nowless and setting inclination of the setting of the sett
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Kobamocht, J., Sillroy C., Starb, D. and Sarrycki, R.
Analyses of the Chiamydomonas reinhardtil Genome: A Hood.,
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Vascular Plants; project phase 2
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Chlamydomonas reinhardtii
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Tel: 919 613 8159
Fax: 919 613 8177
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DCMB Box 91000
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   Conservative
                                                                                        chauser@duke.edu
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몽 8

Matches

Query Match 3.4%; Score 43.2; DB 13; Length 884; Best Local Similarity 16.6%; Prod. No. 3.2;

Conservative 132; Mismatches 149; Indels

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AUTHORS
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becamination of this BAC-end sequence was carried out as part of a
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collaboration with the mercially Throughlit tenome profits

polanes see they./www.fruitfly.cog The BOCP Drouphila

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for the library is named merci seed to the BOCP profits

Mr. The library is named merci seed to constructed by partial

ECOSE dispersion of Docsophila DAA provided by the BOCP from the

pagenic Striam yir on be p. the same service used for the library or

pand Bor to order individual BAC clones, the ontire library, or

force the striat of the BOCPA Resource Conter can be

found at http://bacpac.med.bufilo.com/drouphila.bac.htm.
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BACR14N21 of RPCI-98 library from Drosophila melanogaster (f
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.f.
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Enkaryota: Metagoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota: Menoptera; Endopteryota; Diptera; Brachycera;
Macomorpha; Enhydroidea; Drosophilidae; Drosophila.

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	759		343		Query Match 3.2%; Score 41.8; DB 13; Length 11 Best Local Similarity 16.8%; Pred. No. 7.5; Matches 69; Conservative 164; Mismatches 182; Indels	/note="end: SP6" 254 a 176 c 160 g 152 t	/organism-"Drosophila /plasmid-"peloBACLI" /plasmid-"peloBACLI" /db_wref-"taxon:7227" /clone_lib-"brosBAC" /clone="BACN37LOB"	rce	library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC	. 6		MEIN	NO NO		7	678 GCGCSCSCGCSCGCG	819 738	798	759	george de la companya
	759		343	639	Ouery Match 3.2%; Score 41.8; DB 13; Length 1101; Best Local Similarity 15.6%; Prod. No. 7.5; Matches 69; Conservative 164; Mismatches 182; Indels 0;	/note="end: SP6" 254 a 176 c 160 g 152 t	/organism-"Drosophila /plasmid-"peloBACLI" /plasmid-"peloBACLI" /db_wref-"taxon:7227" /clone_lib-"brosBAC" /clone="BACN37LOB"	rce	library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC	. 6		NISM Plasmid Dr. Eukaryota; Pterygota;	NO NO	Drosophila melanogaster genome survey sequence SP6 BACN37LO8 of DrosBAC library from Drosophila melano fly), genomic survey sequence.	7	678 GCGCSCSCGCSCGCG	8.9 cgggccggtggactaccagcagtaggtaaccgrotgggtaccggtatcggtattggaaagg 7.8 CGGGSCCGSCCSCCCSCCSGGMSSCCWCSGGMSSCCWCSCGMSCCMSCCMSCCMSCCMSCCMSSCSSSSS	798 GMGMGCACACACGCGMSHMGAGRGSGGGAMCAGVGGMSCGGGRCRSGCCYCVCMGCGGAG	030 MARKUMTSUANSUKUSUKUGUSUKUKUKUKUKUKUKUKUANGRENGRYGNGCACAC 759 taatqetqqeaqqtettaacoqttcqtcaccaccacaaaaaaactacaaaaaaccaccaaaaaaccacc	george de la companya

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Best Local Similarity 57.8%;
Matches 74; Conservative
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Tel: 919 613 8159
Fax: 919 613 8177
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1 (bases 1 to 737)
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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963961EIL2, V. C. reinhardtii CC-1690, Stress condition I, normalized
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA seguence.
                                                                                                               TAT 9
                                                                                                      chauser@duke.edu
                                                                                                                                                                                                                                                                                                                            /strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690,
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                         0; Mismatches
                                       Score 41.6;
Pred. No. 7.
                                                         DB 11;
                            54;
                            THORIS
                                                      Length 737;
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704 gtmatggtctgagccagctccttggcmacggggga 738
                                                              644 ccgaaggcgagcagaacgcctataaaaaaaggagtcactgatgcgctgtcgggcctgatgg 703
                                                                                                                     584 gcctgtttggtgatgggcaggtggcacccagggcagttcctctgggggcaagcagccga 643
                                                                                                   328 GTCAGAGTGCTGGGAGAGAACTGGGCCAAGGGGCACTACAGAGAGGCGCGGAGCTGG 387
                                             388 TGGACTCGGTGCTGGATGTCGTGAGAACAGGAGGCTGAGCAGCTGTGACTGCCCTGCACG
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506 octooggcacagattocacotcagactocagogacocgatgcagcagotgctgaagatgt 565

84;

Conservative

0; Mismatches

Score 41.4; DB 11; Length 894; Pred. No. 8.9; 71; Indels

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Location/Qualifiers
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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602708514F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4845074 5',
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/db_xref="taxon:9606"
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	Qy 358 ganggactgtcgaacgctgtaacgatatgttaggcggttcgctgaacacgctgggctcg 417	Qy 298 atgggcggtggcttaggctggcttaggctaggttaggtt	Oy 238 otgocigottactcaccggcatgatgatgatgatgatgatgatgatgggcggtggtggctg 297 Db 649 KCKKKKKKKKKNNKNNNNNNNNNNNNNNNNNNNNNKKKOKKKKKK	Oy 178 ttggstgscaattctgcattgsgsctgsgsgsgsgtaatcaaaaatgataccgtcaatpag 237 Db 709 KOKNKKKHKNNNOKNNKKKKKKKKKKKKKKKKKKOKNGKKNKONONKKNNOHONNKKNNNOKKK 650	Oy 118 tratacygcygrycygogyanatancygrttgytygyraccagracyccagaatgotygg 177 Db 769 CAKDCHMENKACHKWCKKBANKKKCDDKCKDCHANWRAANAKACHKWCDKCGKKGKKN 710	Oy 56 taagaggaatkogttatgagtctgattacaapttaggctggaggcancgatggaaatt 117 bb 829 YACKHBKRWYBKBCHAKACHTCKCBNYKKCTKKAAANKBKWAKABKNKKKDCKAMCACH 770	Query Match 3.2%; Score 41.2; DB 13; Length 1101; Best Local Similarity 8.4%; Pred. No. 11; Matches 32; Conservative 134; Mismatches 216; Indels 0;	/CLORE_LID-PORSBAC* //CLORE***BACHISIDS* 80 c 146 g 113 t 540 others ORIGIN	**************************************	http://www. library.() d'Etude di project g and Genev pBeloBACL	COMMENT Determination with the European Drosophila Gename Projector Collaboration with Collaboratio	SEL GE	ORGANISM Plannid Drosophila melanogaster Tacheata; Hexapoda; Insecta; Eskaryota; Metazoa; Arthropoda; Tacheata; Hexapoda; Insecta; Erecyyota; Moyera; Endepear; Endoperayota; Dipkera; Brachycear; Erecyyota; Moyerapha; Ephydrolea; Drosophildae; Drosophila.	ACCESSION ALIOSON GISCAURIC SULPREY SEQUENCE. VERSION ALIOSON GISCAURIC SULPREY SEQUENCE. KEYMORDS GISCAURIC GISCAURIC SULPREY SULPREY GISCAURIC SULPREY GIS	RESULT 10 CMSO16LM/c CMSO16LM 1101 bp DAN GSS 25-JUL-1999 DEFINITION Drosophila melanogaster genome survey sequence 77 and of BAC ACQUISTION Drosophila melanogaster for propophila melanogaster (for propophila melanogast	Db 448 GTTTCCAGCTGACCCACATCCCTGGGTAGGGAGGA 482
K 470 ESSITA 12 COSTISS CHS01258 1101 bp DNA GSS 26-UU-1999	Db	рь 222 Оу 630	dq VD	pest Local Similarity 52.79, Pred. No. 10, Matches 89; Conservative 0; Missatches 80, Marches 60, Sin ogganospaticosnoticaganicosganocyatignagos; Oy 510 ogganospaticosnoticaganicosganocyatignagos;	Query Match 3.2%;	BASE COUNT 143	antible (Message of Lord and He medium bubbled with % CoX. partible (Message of Lord and He medium bubbled with % CoX. partible (Message of Lord and A	Anche-Wester: phissorphy II SF, Site, Booki, Site, 3: Anche-Wester: phissorphy II SF, Site, 1: Booki, Site, 3: Anche-Wester: Constructed by John Backet and Guffery Mail-Sep Passe in Tap (Restaure-contailing) medium in the Light. Tap exists in it be gath; Site (schimbal) medium in	E2333	FEATURES Source	COMMENT	TITLE Analyses of the Chiamydomons reinhardtid Gonzey Unicellular System for Analyzing Gene Function and Wascular Plants; project phase 5	ORGANISM REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE	1199 RESULT; 11 RESULT; 12 RESULT; 13 RESULT; 13 RESULT; 13 RESULT; 14 RESULT; 14 RESULT; 15 R	Db 469 KKKKKKKANNINNCIKKKCCINIKK 448

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Betenination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosphila Gender Project (EDDP)

http://www.edgp.ed.lac.uit. "his Drosphila melanopaster BAC
Library (from BAC) was made by Alain filling at CEPH (Centre
of Fixude out Polymorphisme Beauth) with funding project grant. The DNA was preserved from embryony
project grant. The DNA was preserved from embryony
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man-learning the Paylan. It has been constructed in the vector
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BP 191 91006 EVRY cedex - FRANCE (8-mail : segref@genoscope.cns.fi
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Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR26H16 of RPCI-98 library from Drosophila melanogaster (fruit 04-JUN-1999

Eukaryota; Metazoā; Arthropoda; Tracheata; Hexapoda; Insecta; Pterryota; Neoptera; Endopteryota; Diptera; Erachyoera; Muscomorpha; Ephydroidea; Drosophilidee; Drosophila.

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : Bp 391 91006 EVEY codex - PRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Common : Web : www.genoscope.cns.fr - Common : www.genos

conincipation with the Marshall General Project (doily). The MODF is constructing a physical map of the Droslophila management general mainst these Mess, Now Intrinse phinometric mattern sections using these Mess, Now Intrinse phinometric mattern sections and the Company of the Company of the Company of the Company and Asron Manager in Picture do Jong's laboratory in the Department of Kangar Jenetics at the Reperty is and west contracted by the Mode From the Kangar Company of the Company of the Mode From the Mode is a considered to the Mode in the Mode in the Mode is a considered to the Mode in the Mode in the Mode is a considered to the Mode in the Mode and the Mode is a considered to the Mode in the Mode and the Mode is a considered to the Mode in the Mode and the Mode is a considered to the Mode and M

/organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone_ib="refoi-98" /clone="BACR26H16" 180 t 235 others

Conservative 123; Mismatches Score 40; DB 13; Pred. No. 20; 118; Inders Length 939 ç Gaps

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Muscomorpha; Enhydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster genome survey sequence TET3 end of BAC.
BACR32D23 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                   700 AKTADKTKK 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 3.1%; Score 39.8;
Local Similarity 44.7%; Pred. No. 20;
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kommanlai; Ethoria; Prizantes; Cotarrini; Hominidae; Nomo.
1, 04a; Gruber; O. Jassee, J. and Folayes; D.
1,1 4a; Gruber; O. Jassee, J. and Folayes; D.
Fall:
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BP 191 91006 EVRY cedex - France
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a 60 c 320 g 28 t 71
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                        4
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                              2002, 04:03:43
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760 KKGKDWTKGTKWDTKTKTKGKKTGSGGGKKKTKYKGTKKTWWAAWKAKKTKKTTKKKGTG 701
                                                      357 cgaaggactgtcgaacgctgaacgatatgttaggcggttcgctgaacacgctgggctc 416
```

AL566993 LTI_FL013_FBrnl Homo sapiens cDNA clone CSODF028YF02

de Sequencage

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers

/clone_lib="LfT_FL013_FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
/lab_host="DM108"

'notee 'Organ: Fetal brain; Wector: pCMVSPORT 6: lat strand CDM, was primed with a Worlf-O-ligo(ET) primer. Five prime end enriched, double-stranded cDWA was digested with Not I and cloned into the Not I and Exo My sites of the pCMVSPORT 6 Vector. Library was constructed by Life

pg/WRSP08T 6 vector. Library was constructed by Life Technologies, contact: reng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email:

78 others

DB 10; Length 631; 70; Indels 0; Gaps

270 gatgagcatgatgggtggtgggtggctgatgggtggcttaggtaa 329

330 tggcttgggtggctcaggtggcctgggcgaaggactgtcgaacgcgctgaacgatatgtt 389

390 aggcggttcgctgaacacgctgggctcgaaaggcggcaa 428

